

SEQUENCE LISTING

<110> Rock, Charles O
Heath, Richard J

<120> Novel Enoyl Reductases and Methods of Use Thereof

<130> SJ-0022

<140> US 09/498,520

<141> 2000-02-04

<160> 62

<170> PatentIn version 3.1

<210> 1

<211> 975

<212> DNA

<213> Streptococcus pneumoniae

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gaactggctg aaaaatgtc cttaaagcaa gaagatcgtt atttgaaaat ctttgcacaa	780
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<212> PRT

<213> Streptococcus pneumoniae

<400> 2

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Ser Lys Ala Gly Gly Leu Gly Ile Ile Gly Gly Asn Ala Pro Lys
35 40 45

Glu Val Val Lys Ala Asn Ile Asp Lys Ile Lys Ser Leu Thr Asp Lys
50 55 60

Pro Phe Gly Val Asn Ile Met Leu Leu Ser Pro Phe Val Glu Asp Ile
65 70 75 80

Val Asp Leu Val Ile Glu Glu Gly Val Lys Val Val Thr Thr Gly Ala
85 90 95

Gly Asn Pro Ser Lys Tyr Met Glu Arg Phe His Glu Ala Gly Ile Ile
100 105 110

Val Ile Pro Val Val Pro Ser Val Ala Leu Ala Lys Arg Met Glu Lys
115 120 125

Ile Gly Ala Asp Ala Val Ile Ala Glu Gly Met Glu Ala Gly Gly His
130 135 140

Ile Gly Lys Leu Thr Thr Met Thr Leu Val Arg Gln Val Ala Thr Ala
145 150 155 160

Ile Ser Ile Pro Val Ile Ala Ala Gly Ile Ala Asp Gly Glu Gly
165 170 175

Ala Ala Ala Gly Phe Met Leu Gly Ala Glu Ala Val Gln Val Gly Thr
180 185 190

Arg Phe Val Val Ala Lys Glu Ser Asn Ala His Pro Asn Tyr Lys Glu
195 200 205

Lys Ile Leu Lys Ala Arg Asp Ile Asp Thr Thr Ile Ser Ala Gln His
210 215 220

Phe Gly His Ala Val Arg Ala Ile Lys Asn Gln Leu Thr Arg Asp Phe
225 230 235 240

Glu' Leu Ala Glu Lys Asp Ala Phe Lys Gln Glu Asp Pro Asp Leu Glu
245 250 255

Ile Phe Glu Gln Met Gly Ala Gly Ala Leu Ala Lys Ala Val Val His
260 265 270

Gly Asp Val Asp Gly Gly Ser Val Met Ala Gly Gln Ile Ala Gly Leu
275 280 285

Val Ser Lys Glu Glu Thr Ala Glu Glu Ile Leu Lys Asp Leu Tyr Tyr
290 295 300

Gly Ala Ala Lys Lys Ile Gln Glu Glu Ala Ser Arg Trp Thr Gly Val
 305 310 315 320

Val Arg Asn Asp

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<213> Streptococcus mutans
  
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<400> 4

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 20 25 30

Ser Lys Ala Gly Gly Leu Gly Ile Ile Gly Gly Asn Ala Pro Lys
 35 40 45

Glu Val Val Lys Ala Asn Ile Asp Lys Ile Lys Ala Val Thr Asn Lys
 50 55 60

Pro Phe Gly Val Asn Ile Met Leu Leu Ser Pro Phe Ala Asp Asp Ile
 65 70 75 80

Val Asp Leu Val Ile Glu Glu Gly Val Lys Val Val Thr Thr Gly Ala
 85 90 95

Gly Asn Pro Gly Lys Tyr Ile Glu Arg Phe His Glu Ala Gly Ile Thr
 100 105 110

Val Ile Pro Val Val Pro Ser Val Ala Leu Ala Arg Arg Met Glu Lys
 115 120 125

Leu Gly Ala Asp Ala Val Ile Ala Glu Gly Met Glu Ala Gly Gly His
 130 135 140

Ile Gly Lys Leu Thr Thr Met Thr Leu Val Arg Gln Val Val Asp Ala
 145 150 155 160

Val Asn Ile Pro Val Ile Gly Ala Gly Val Ala Asp Gly Arg Gly
 165 170 175

Ala Ala Ala Val Phe Met Leu Gly Ala Glu Ala Ile Gln Val Gly Thr
 180 185 190

Arg Phe Ala Val Ala Lys Glu Ser Asn Ala His Ala Asn Phe Lys Lys
195 200 205

Lys Ile Leu Lys Ala Lys Asp Ile Asp Thr Val Ile Ser Ala Ser Ile
210 215 220

Val Gly His Pro Val Arg Ala Ile Lys His Lys Leu Ser Ser Ala Tyr
 225 230 235 240

Ala Thr Ala Glu Lys Glu Phe Leu Arg Gly Glu Lys Ser Gln Glu Asp
245 250 255

Ile Glu Val Leu Gly Ala Gly Ala Leu Arg Asn Ala Val Val Asp Gly
260 265 270

Asp Val Asp Asn Gly Ser Val Met Ala Gly Gln Ile Ala Gly Phe Val
275 280 285

Thr Lys Glu Glu Thr Cys Glu Glu Ile Leu Lys Asp Leu Tyr Tyr Gly
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<212> DNA
<213> *Streptococcus pyogenes*

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<212> PRT
<213> Streptococcus pyogenes

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			20					25				30			

Ser	Asn	Ala	Gly	Gly	Leu	Gly	Ile	Ile	Gly	Gly	Asn	Ala	Pro	Lys
35							40					45		

Glu	Val	Val	Lys	Ala	Asn	Ile	Asp	Arg	Val	Lys	Ala	Ile	Thr	Asp	Arg
50						55				60					

Pro	Phe	Gly	Val	Asn	Ile	Met	Leu	Leu	Ser	Pro	Phe	Ala	Asp	Asp	Ile
65						70				75			80		

Val	Asp	Leu	Val	Ile	Glu	Glu	Val	Lys	Val	Val	Thr	Thr	Gly	Ala
					85				90			95		

Gly	Asn	Pro	Gly	Lys	Tyr	Met	Glu	Arg	Leu	His	Gln	Ala	Gly	Ile	Ile
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Leu	Gly	Val	Asp	Ala	Val	Ile	Ala	Glu	Gly	Met	Glu	Ala	Gly	Gly	His
						130		135			140				

Ile	Gly	Lys	Leu	Thr	Thr	Met	Ser	Leu	Val	Arg	Gln	Val	Val	Glu	Ala
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Val Ser Ile Pro Val Ile Ala Ala Gly Gly Ile Ala Asp Gly His Gly
165 170 175

Ala Ala Ala Ala Phe Met Leu Gly Ala Glu Ala Val Gln Ile Gly Thr
 180 185 - 190

Arg Phe Val Val Ala Lys Glu Ser Asn Ala His Gln Asn Phe Lys Asp
195 200 205

Lys Ile Leu Ala Ala Lys Asp Ile Asp Thr Val Ile Ser Ala Gln Val
 210 215 220

Val Gly His Pro Val Arg Ser Ile Lys Asn Lys Leu Thr Ser Ala Tyr
 225 230 235 240

Ala Lys Ala Glu Lys Ala Phe Leu Ile Gly Gln Lys Thr Ala Thr Asp
245 250 255

Ile Glu Glu Met Gly Ala Gly Ser Leu Arg His Ala Val Ile Glu Gly
260 265 270

Asp Val Val Asn Gly Ser Val Met Ala Gly Gln Ile Ala Gly Leu Val
275 280 285

Arg Lys Glu Glu Ser Cys Glu Thr Ile Leu Lys Asp Ile Tyr Tyr Gly
290 295 300

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305 . . . 310 . . . 315 . . . 320

Ile Glu Lys

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<211> 1068
<212> DNA
<213> Staphylococcus aureus COL

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ggcacaatag ggcgcagggtta cttaataacg cagcaattgg aagatgaaat agatattgtta 180
cgccaaattaa cgtcaaatttc ttggcgtta aatgtctttg taccaaagtca acaatcatat 240
accagtagtc aaattgaaaa tatgaatgcg tggtaaaac cttatcgacg cgccattacat 300
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ataagcagggt tgaagcagc gatatgtcaa cttaggttgc cagcaacaag tggtgtatgg	480
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ggacatcggtt gttcattttt aaaaacctaaa aatcaattac ctatggttgg aacaatataat	600
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gatggtagag gagtttggc aagtattgtc ttatgttgc aaggggtaca aatggggcacc	720
gcatttttaa catcacaaga cagtaatgtc tcagaactac tgcgagatgc aattataat	780
agtaaagaaa cagatacagt cattacaaaa gcgtttagt gaaagcttgc acgcggatc	840
aacaatagggtt ttatgttgc aatgttccaa tacgttgc aatcccaata ttatccaaata	900
caaaatggc taacaatgtt cataaaaaaa gcccgcacaa acatggcga caaagatgtt	960
atacatatgtt gggttggaca aagccgcga ctgttgcacaa cgcatccgc caacaccatc	1020
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<211> 355
<212> PRT
<213> Staphylococcus aureus COL

<400> 8

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Ser Val Ser Asn Ser Gly Gly Leu Gly Thr Ile Gly Ala Gly Tyr Phe		
35	40	45

Asn Thr Gln Gln Leu Glu Asp Glu Ile Asp Tyr Val Arg Gln Leu Thr		
50	55	60

Ser Asn Ser Phe Gly Val Asn Val Phe Val Pro Ser Gln Gln Ser Tyr			
65	70	75	80

Thr Ser Ser Gln Ile Glu Asn Met Asn Ala Trp Leu Lys Pro Tyr Arg		
85	90	95

Arg Ala Leu His Leu Glu Glu Pro Val Val Lys Ile Thr Glu Glu Gln		
100	105	110

Gln Phe Lys Cys His Ile Asp Thr Ile Ile Lys Lys Gln Val Pro Val
115 120 125

Cys Cys Phe Thr Phe Gly Ile Pro Ser Glu Gln Ile Ile Ser Arg Leu
130 135 140

Lys Ala Ala Asn Val Lys Leu Ile Gly Thr Ala Thr Ser Val Asp Glu
145 150 155 160

Ala Ile Ala Asn Glu Lys Ala Gly Met Asp Ala Ile Val Ala Gln Gly
165 170 175

Ser Glu Ala Gly Gly His Arg Gly Ser Phe Leu Lys Pro Lys Asn Gln
180 185 190

Leu Pro Met Val Gly Thr Ile Ser Leu Val Pro Gln Ile Val Asp Val
195 200 205

Val Ser Ile Pro Val Ile Ala Ala Gly Gly Ile Met Asp Gly Arg Gly
210 215 220

Val Leu Ala Ser Ile Val Leu Gly Ala Glu Gly Val Gln Met Gly Thr
225 230 235 240

Ala Phe Leu Thr Ser Gln Asp Ser Asn Ala Ser Glu Leu Leu Arg Asp
245 250 255

Ala Ile Ile Asn Ser Lys Glu Thr Asp Thr Val Ile Thr Lys Ala Phe
260 265 270

Ser Gly Lys Leu Ala Arg Gly Ile Asn Asn Arg Phe Ile Glu Glu Met
275 280 285

Ser Gln Tyr Glu Gly Asp Ile Pro Asp Tyr Pro Ile Gln Asn Glu Leu
290 295 300

Thr Ser Ser Ile Arg Lys Ala Ala Ala Asn Ile Gly Asp Lys Glu Leu
305 310 315 320

Ile His Met Trp Ser Gly Gln Ser Pro Arg Leu Ala Thr Thr His Pro
325 330 335

Ala Asn Thr Ile Met Ser Asn Ile Ile Asn Gln Ile Asn Gln Ile Met
340 345 350

Gln Tyr Lys
355

Met Lys Cys Thr Tyr Leu Arg Thr Lys Gly Arg Ile Lys Ser Met Asn
1 5 10 15

Gln Glu Leu Cys Glu Leu Leu Gly Ile Asn Tyr Pro Ile Phe Gln Gly
20 25 30

Gly Met Ala Trp Val Ala Asp Ala Ser Leu Ala Ser Ala Val Ser Asn
 35 40 45

Ala Gly Gly Leu Gly Ile Ile Ala Gly Gly Asn Ala Pro Lys Glu Val
 50 55 60

Val Lys Lys Glu Ile Lys Lys Val Lys Glu Leu Thr Glu Gln Pro Phe
 65 70 75 80

Gly Val Asn Ile Met Leu Leu Ser Pro Phe Ala Asp Glu Ile Val Asp
 85 90 95

Leu Val Cys Glu Glu Gin Val Pro Val Val Thr Thr Gly Ala Gly Asn
 100 105 110

Pro Ala Lys Tyr Met Ala Arg Phe Lys Glu His Asn Ile Lys Val Ile
 115 120 125

Pro Val Val Pro Ser Val Ala Leu Ala Lys Arg Met Glu Lys Ile Gly
 130 135 140

Ala Asp Ala Val Ile Phe Glu Gly Met Glu Ala Gly Gly His Ile Gly
 145 150 155 160

Lys Leu Thr Thr Met Ser Gly Leu Pro Gln Ile Val Asp Ala Val Ser
 165 170 175

Ile Pro Val Ile Ala Ala Gly Gly Ile Gly Asp Gly Arg Gly Met Ala
 180 185 190

Ala Ala Phe Met Leu Gly Ala Glu Ala Val Gln Leu Gly Thr Arg Phe
 195 200 205

Leu Ile Ala Lys Glu Cys Asn Val His Pro Asp Tyr Lys Gln Lys Val
 210 215 220

Leu Lys Ala Arg Asp Leu Asp Ala Val Ile Thr Cys Gln His Phe Gly
 225 230 235 240

His Pro Val Arg Thr Leu Lys Asn Lys Leu Thr Ala Gln Tyr Asn Gln
 245 250 255

Leu Glu Lys Gln Glu Leu Gln Lys Glu Val Pro Asp Leu Glu Met Phe
 260 265 270

Glu Lys Ile Gly Gln Gly Ala Leu Arg Lys Ala Val Val Asp Gly Asp

275

280

285

Met Asp Tyr Gly Ser Val Met Ala Gly Gln Ile Ala Gly Leu Ile Lys
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Lys Glu Glu Thr Ala Gln Glu Ile Ile Asp Ser Leu Met Ser Glu Cys
 305 310 315 320

Lys Ala Ile Val His Lys Met Asn Gln Arg Trp Gly
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<210> 11
 <211> 933
 <212> DNA
 <213> Clostridium acetobutylicum

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 <211> 310
 <212> PRT
 <213> Clostridium acetobutylicum

<400> 12

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 20 25 30

Val Ser Asn Ala Gly Gly Leu Gly Ile Ile Ala Ala Asn Ala Pro
 35 40 45

Val Glu Tyr Val Arg Asp Glu Ile Arg Lys Ala Lys Lys Leu Thr Asp
 50 55 60

Lys Pro Phe Gly Val Asn Ile Met Leu Leu Ser Asp Asn Ala Glu Glu
 65 70 75 80

Val Ala Lys Met Val Cys Glu Glu Gly Val Lys Val Val Thr Thr Gly
 85 90 95

Ala Gly Asn Pro Gly Lys Tyr Ile Asp Met Trp Lys Glu His Asp Ile
 100 105 110

Lys Val Ile Pro Val Val Ala Ser Val Ala Leu Ala Arg Arg Met Glu
 115 120 125

Arg Cys Gly Val Asp Ala Val Val Ala Glu Gly Cys Glu Ser Gly Gly
 130 135 140

His Val Gly Glu Leu Thr Thr Met Ala Leu Val Pro Gln Val Val Asp
 145 150 155 160

Ala Ile Asn Ile Pro Val Ile Ala Ala Gly Gly Ile Gly Asp Gly Arg
 165 170 175

Gly Val Ala Ala Ala Phe Ala Leu Gly Ala Ser Gly Val Gln Val Gly
 180 185 190

Thr Arg Phe Leu Ile Ala Lys Glu Cys Thr Val His Gln Asn Tyr Lys
 195 200 205

Asn Lys Val Leu Lys Ala Lys Asp Ile Asp Thr Glu Val Thr Gly Arg
 210 215 220

Ser Thr Gly His Pro Val Arg Val Leu Arg Asn Lys Leu Ala Arg Lys
 225 230 235 240

Tyr Lys Leu Met Glu Lys Glu Gly Ala Ser Pro Glu Glu Met Glu Glu

14

245

250

255

Leu Gly Arg Gly Ala Leu Pro Arg Ala Val Arg Glu Gly Asp Val Asp
 260 265 270

Asn Gly Ser Val Met Ala Gly Gln Ile Ala Gly Leu Ile Asn Lys Glu
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Glu Thr Cys Asp Glu Ile Val Glu Ser Met Phe Lys Glu Ala Val Glu
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Val Ile Asp Arg Ile Lys
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<210> 13
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 <212> DNA
 <213> Clostridium difficile

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gctatggtaa aagaaataac accttggtaag gaaattatag aggctatggtaa aatcaagca	900	
agagagatttta tgccagcaat agaactgttaa	930	

<210> 14
 <211> 309
 <212> PRT

<213> Clostridium difficile

<400> 14

Met	Asn	Lys	Ile	Cys	Lys	Ile	Leu	Asn	Ile	Lys	Tyr	Pro	Val	Ile	Gln
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Gly	Gly	Met	Ala	Trp	Val	Ala	Thr	Ala	Ser	Leu	Ala	Ser	Ala	Val	Ser
									20			25		30	

Asn	Ala	Gly	Gly	Leu	Gly	Ile	Ile	Ala	Ala	Gly	Asn	Ala	Pro	Lys	Glu
									35			40		45	

Ala	Ile	Lys	Lys	Glu	Ile	Val	Glu	Cys	Lys	Lys	Leu	Thr	Asp	Lys	Pro
									50			55		60	

Phe	Gly	Val	Asn	Val	Met	Leu	Met	Ser	Pro	Phe	Val	Asp	Asp	Ile	Ile
65									70			75		80	

Asp	Leu	Ile	Ile	Glu	Glu	Lys	Val	Gln	Val	Ile	Thr	Thr	Gly	Ala	Gly
									85			90		95	

Asn	Pro	Ala	Lys	Tyr	Met	Asp	Arg	Leu	Lys	Glu	Ala	Gly	Thr	Lys	Val
									100			105		110	

Ile	Pro	Val	Val	Pro	Thr	Ile	Ala	Leu	Ala	Gln	Arg	Met	Glu	Lys	Leu
									115			120		125	

Gly	Ala	Thr	Ala	Val	Ile	Ile	Ala	Glu	Gly	Thr	Glu	Gly	Gly	His	Ile
									130			135		140	

Gly	Glu	Leu	Thr	Thr	Met	Val	Leu	Val	Pro	Gln	Val	Ala	Asp	Ala	Val
145									150			155		160	

Asn	Ile	Pro	Val	Ile	Ala	Ala	Gly	Ile	Val	Asp	Gly	Arg	Gly	Ile	
									165			170		175	

Ala	Ala	Ser	Phe	Ala	Leu	Gly	Ala	Ser	Ala	Val	Gln	Val	Gly	Thr	Arg
									180			185		190	

Phe	Ile	Cys	Ser	Glu	Glu	Cys	Ser	Val	His	Ser	Asn	Tyr	Lys	Asn	Leu
									195			200		205	

Val	Leu	Lys	Ala	Lys	Asp	Arg	Asp	Ala	Ile	Val	Thr	Gly	Arg	Ser	Thr
									210			215		220	

Gly	His	Pro	Val	Arg	Thr	Leu	Lys	Asn	Lys	Leu	Ser	Lys	Glu	Phe	Leu
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225

230

235

240

Lys Met Glu Gln Asn Gly Ala Thr Pro Glu Glu Leu Asp Lys Lys Gly
 245 250 255

Thr Gly Ala Leu Arg Phe Ala Thr Val Asp Gly Asp Ile Glu Lys Gly
 260 265 270

Ser Phe Met Ala Gly Gln Ser Ala Ala Met Val Lys Glu Ile Thr Pro
 275 280 285

Cys Lys Glu Ile Ile Glu Ala Met Val Asn Gln Ala Arg Glu Ile Met
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Pro Ala Ile Glu Leu
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<210> 15
 <211> 873
 <212> DNA
 <213> Porphyromonas gingivalis W83

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ggtgcggat ccatgcattt ggacaatctg gagcatcaca tccgttctgtt taaagctgtt	180
acagacaagg ctttcgggtt gaaatgttcc ttcttctatc cggagatggaa caaaatcatg	240
gaggattatca tgaggaaaca tggccgtt gttgttacgtt cggccgttag tccaaagggtt	300
tggacagcca agttgttacgtt tggccgttacgtt aaggttatacgtt atgttagttagt cagtgccaca	360
ttcgtctcgca aatcagaggc acggccgttacgtt gacgcctatcg tggccgttacgtt gttgttacgtt	420
ggccggacata atggacgaga ggagactacg acccttctgtt tgataacctgtt agttagtggat	480
gctgttacgtt ttcctgttacgtt tgctgttacgtt gggatgttacgtt cggccgttacgtt agttgttacgtt	540
gttttggctt tgggttacgtt tgctgttacgtt gttttgttacgtt gttttgttacgtt gttttgttacgtt	600
atgttggccgtt atgttggccgtt atgttggccgtt atgttggccgtt atgttggccgtt atgttggccgtt	660
atgttggccgtt atgttggccgtt atgttggccgtt atgttggccgtt atgttggccgtt atgttggccgtt	720
atgttggccgtt atgttggccgtt atgttggccgtt atgttggccgtt atgttggccgtt atgttggccgtt	780
atgttggccgtt atgttggccgtt atgttggccgtt atgttggccgtt atgttggccgtt atgttggccgtt	840
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<210> 16

<211> 313
<212> PRT
<213> Porphyromonas gingivalis W83
<400> 16

Met Asn Arg Ile Cys Glu Leu Leu Gly Ile Glu His Pro Ile Ile Ser
1 5 10 15

Gly Gly Met Val Trp Cys Ser Gly Trp Lys Leu Ala Ser Ala Val Ser
20 25 30

Asn Cys Gly Gly Leu Gly Leu Ile Gly Ala Gly Ser Met His Pro Asp
35 40 45

Asn Leu Glu His His Ile Arg Ser Cys Lys Ala Ala Thr Asp Lys Pro
50 55 60

Phe Gly Val Asn Val Pro Leu Leu Tyr Pro Glu Met Asp Lys Ile Met
65 70 75 80

Glu Ile Ile Met Arg Glu His Val Pro Val Val Val Thr Ser Ala Gly
85 90 95

Ser Pro Lys Val Trp Thr Ala Lys Leu Lys Ala Ala Gly Ser Lys Val
100 105 110

Ile His Val Val Ser Ser Ala Thr Phe Ala Arg Lys Ser Glu Ala Ala
115 120 125

Gly Val Asp Ala Ile Val Ala Glu Gly Phe Glu Ala Gly Gly His Asn
130 135 140

Gly Arg Glu Glu Thr Thr Thr Leu Cys Leu Ile Pro Glu Val Val Asp
145 150 155 160

Ala Val Asn Ile Pro Val Val Ala Ala Gly Gly Ile Ala Ser Gly Arg
165 170 175

Ala Val Ala Ala Ala Leu Ala Leu Gly Ala Asp Ala Val Gln Val Gly
180 185 190

Thr Arg Phe Ala Leu Ser Glu Glu Ser Ser Ala His Glu Asp Phe Lys
195 200 205

Ala His Cys Arg Arg Ser Val Glu Gly Asp Thr Met Leu Ser Leu Lys
210 215 220

Ala Val Ser Pro Thr Arg Leu Leu Lys Asn Lys Phe Tyr Gln Asp Val
 225 230 235 240

Phe Ala Ala Glu Gln Arg Gly Ala Ser Val Glu Glu Leu Arg Glu Leu
 245 250 255

Leu Gly Arg Gly Arg Ala Lys Gln Gly Ile Phe Glu Gly Asp Leu His
 260 265 270

Glu Gly Glu Leu Glu Ile Gly Gln Ala Val Ser Gln Ile Ser His Ala
 275 280 285

Glu Thr Val Ala Glu Ile Met Val Asp Leu Val Asp Gly Tyr Lys Arg
 290 295 300

Ser Leu Ala Gly Met Pro Thr Glu Ile
 305 310

<210> 17
<211> 966
<212> DNA
<213> Caulobacter crescentus

<400>	17					
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ggcggtctgg	gcatggccgg	caccagcccc	gacttcatecc	gcccggccat	gcgcgaggtc	180
aaaagccctga	ccgacaaagcc	gttcggggtg	gacctgtgg	ccggccacgccc	ggatgcgtctg	240
accgcgtccg	tgcgggtcat	catcgaggag	ggccgcctct	cattttgcgc	gggcgttggcc	300
gtggccctgc	cgatccatcg	acgactcaag	gccgcggggcc	tgaagggtcat	gttcgttgc	360
ggagccgtga	agcacgcgg	caaggccgag	caggccggct	gacgcgcgg	gatctggcaa	420
ggcgccgagg	gccccgttca	cacgggtctc	gtccggcaccc	tgccgcgttgg	ggcccaggcc	480
gtggaggccg	tgaagatccc	ggtgttcgac	gccccggggcc	tgcatgacgg	ccgcgggtcg	540
gccccggggcc	tggctctggg	cgccgcaggcc	gtctggatgg	gcacgcgggtt	catacgccctcg	600
cacgaggccc	atgcggggcga	tcttacccgc	caggccgtgg	tcgaggccgc	cgacgaggac	660
acgggtgcgc	cgccgtctca	ctcgggcaag	ccgatgcggg	tgaagaagaa	cccttatgtc	720
gacgactggg	aagcgcgtcc	cgccgcacatc	cagcccttcc	cgccgcaggcc	catgggttcg	780
atccgcata	gcccgcattgg	cgccatggc	ggccagatcg	aggcccttgg	cgccgcacag	840
tcctgtttcg	ccatggccca	gagccgcggc	ggcggtgcgc	agatcttgc	ggccgcggcag	900

atcgtaaaggc ggctgtatggc cgagggccgag acggcgctgg ccaaggccctc ggccttcagg 960
 acctgaa 966

<210> 18
 <211> 321
 <212> PRT
 <213> Caulobacter crescentus

<400> 18

Met	Gly	Leu	Arg	Thr	Pro	Leu	Cys	Asp	Leu	Leu	Asp	Ile	Glu	His	Pro
1															
														15	

Ile Leu Leu Ala Gly Met Gly Gly Val Ser Tyr Ala Pro Leu Ala Ala
 20 25 30

Ala Val Ser Asn Ala Gly Gly Tyr Gly Val Leu Gly Met Ala Gly Thr
 35 40 45

Ser Pro Asp Phe Ile Arg Ala Gln Met Arg Glu Val Lys Ser Leu Thr
 50 55 60

Asp Lys Pro Phe Gly Val Asp Leu Leu Ala Ala Thr Pro Asp Ala Leu
 65 70 75 80

Thr Ala Ser Val Glu Val Ile Ile Glu Glu Gly Ala Ser Ser Phe Val
 85 90 95

Ala Gly Leu Gly Val Pro Leu Pro Ile Ile Glu Arg Leu Lys Ala Ala
 100 105 110

Gly Leu Lys Val Met Val Val Cys Gly Ala Val Lys His Ala Val Lys
 115 120 125

Ala Glu Gln Ala Gly Cys Asp Ala Val Ile Cys Gln Gly Gly Glu Gly
 130 135 140

Gly Gly His Thr Gly Leu Val Gly Thr Leu Pro Leu Val Ala Gln Ala
 145 150 155 160

Val Glu Ala Val Lys Ile Pro Val Val Ala Ala Gly Gly Leu His Asp
 165 170 175

Gly Arg Gly Leu Ala Ala Ala Leu Ala Leu Gly Ala Gln Gly Val Trp
 180 185 190

Met Gly Thr Arg Phe Ile Ala Ser His Glu Ala His Ala Gly Asp Leu

195	200	205
Tyr Arg Gln Ala Val Val Glu Ala Ala Asp Glu Asp Thr Val Arg Thr		
210	215	220
Arg Cys Tyr Ser Gly Lys Pro Met Arg Val Lys Lys Asn Pro Tyr Val		
225	230	235
Asp Asp Trp Glu Ala Arg Pro Gly Asp Ile Gln Pro Phe Pro Gln Gln		
245	250	255
Ala Met Val Ser Ile Arg Asn Gly Ala Met Gly Gly Ile Gly Gly Gln		
260	265	270
Ile Glu Gly Leu Asp Ala Ala Lys Ser Cys Phe Ala Met Gly Gln Ser		
275	280	285
Ala Gly Gly Val Arg Glu Ile Leu Pro Ala Gly Glu Ile Val Lys Arg		
290	295	300
Leu Met Ala Glu Ala Glu Thr Ala Leu Ala Lys Ala Ser Ala Phe Arg		
305	310	315
320		

Thr

<210>	19					
<211>	987					
<212>	DNA					
<213>	Pseudomonas aeruginosa					
<400>	19					
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ggccgcatgc	agtgggtcgg	ccgtgccgag	atggctgccc	cgggtggccaa	cgccgggtggc	120
ctggcgacgc	tgtccggcgtt	gaccgcggcg	agccccggagg	cactggctgc	ggagatgtcc	180
cgctccgcgg	agctgaccgca	tccggcggttc	ggggtaaacc	tgaccttgct	gcccgcacgc	240
aagccggtgtc	cctatggccga	atatccgcga	gccatcatcg	aggcgaaaat	ccgcgtcgtc	300
gaaaccggccg	gcaacgcaccc	cgccgagcac	atccgcgaat	tccgtgcaca	cgccgtcaag	360
gtgatccaca	agtgcaccgc	cgtgcgcct	cgctcaagg	ccgagcgcact	gggcgtggac	420
gccgtctcca	tgcacgggtt	cgagtgtgccc	ggccacccgg	cgaggacga	catccccggc	480
ctgggtttgc	tgcggccgcg	ggccaaacgg	ctacggcgtgc	cgatcatcg	ctccggcggt	540
tteggcgatg	gacgtggcct	ggtcgccccg	ctggcgctgg	gtgcggacgc	gatcaaacatg	600

ggcacgcgt	tcctggccac	tgcgaatgt	ccgatacacc	ctgcggtaa	ggcgccgatc	660
ctgtcgcccg	acgagcggtc	caccgacctg	atcatcggtt	ccctgcgaa	taccgcgcgg	720
gtggcgcgca	acgcgatcg	ccaggaacta	ctggcgatcg	aggcacgcgg	cgccgcggcg	780
tacgcgatcg	tcgcgcgtcgt	ggtcagcggtc	cagcgcggtc	gccagggtgt	ccagcaggggc	840
gataccgacc	tggggatctg	gtcgccccgc	atggtccagg	gcctgatcga	cgacgaaccgc	900
gcctgcgcgg	agttgcgtcg	ggacatcgtc	gagcaggcgc	gcacaactgg	gcgtcaacgc	960
ctggaggcga	tgctcgccgg	ggtctgta				987

<210> 20

<211> 328

<212> PRT

<213> Pseudomonas aeruginosa

<400> 20

Met	Gly	Val	Phe	Arg	Thr	Arg	Phe	Thr	Glu	Thr	Phe	Gly	Val	Glu	His
1															
														10	15

Pro	Ile	Met	Gln	Gly	Gly	Met	Gln	Trp	Val	Gly	Arg	Ala	Glu	Met	Ala
														20	30

Ala	Ala	Val	Ala	Asn	Ala	Gly	Gly	Leu	Ala	Thr	Leu	Ser	Ala	Leu	Thr
														35	45

Gln	Pro	Ser	Pro	Glu	Ala	Leu	Ala	Ala	Glu	Ile	Ala	Arg	Cys	Arg	Glu
														50	60

Leu	Thr	Asp	Arg	Pro	Phe	Gly	Val	Asn	Leu	Thr	Leu	Leu	Pro	Thr	Gln
														65	80

Lys	Pro	Val	Pro	Tyr	Ala	Glu	Tyr	Arg	Ala	Ala	Ile	Ile	Glu	Ala	Gly
														85	95

Ile	Arg	Val	Val	Glu	Thr	Ala	Gly	Asn	Asp	Pro	Gly	Glu	His	Ile	Ala
														100	110

Glu	Phe	Arg	Arg	His	Gly	Val	Lys	Val	Ile	His	Lys	Cys	Thr	Ala	Val
														115	125

Arg	His	Ala	Leu	Lys	Ala	Glu	Arg	Leu	Gly	Val	Asp	Ala	Val	Ser	Ile
														130	140

Asp	Gly	Phe	Glu	Cys	Ala	Gly	His	Pro	Gly	Glu	Asp	Asp	Ile	Pro	Gly
														145	155

Leu Val Leu Leu Pro Ala Ala Ala Asn Arg Leu Arg Val Pro Ile Ile
 165 170 175

Ala Ser Gly Gly Phe Ala Asp Gly Arg Gly Leu Val Ala Ala Leu Ala
 180 185 190

Leu Gly Ala Asp Ala Ile Asn Met Gly Thr Arg Phe Leu Ala Thr Arg
 195 200 205

Glu Cys Pro Ile His Pro Ala Val Lys Ala Ala Ile Arg Ala Ala Asp
 210 215 220

Glu Arg Ser Thr Asp Leu Ile Met Arg Ser Leu Arg Asn Thr Ala Arg
 225 230 235 240

Val Ala Arg Asn Ala Ile Ser Gln Glu Val Leu Ala Ile Glu Ala Arg
 245 250 255

Gly Gly Ala Gly Tyr Ala Asp Ile Ala Ala Leu Val Ser Gly Gln Arg
 260 265 270

Gly Arg Gln Val Tyr Gln Gln Gly Asp Thr Asp Leu Gly Ile Trp Ser
 275 280 285

Ala Gly Met Val Gln Gly Leu Ile Asp Asp Glu Pro Ala Cys Ala Glu
 290 295 300

Leu Leu Arg Asp Ile Val Glu Gln Ala Arg Gln Leu Val Arg Gln Arg
 305 310 315 320

Leu Glu Gly Met Leu Ala Gly Val
 325

<210> 21
 <211> 1044
 <212> DNA
 <213> Bacillus subtilis

<400> 21						
atgaatgaat ttatgaaaaa gttttcttta acaaaaacgc ttattcaaggc tccaaatggct	60					
ggcggttata caaagccccg acttgcatct gcagtttgcg atcaagggtc ttttggcagc	120					
ttagcatcg ggtatcttac gccagacctc ctagaacaac aaataaaaaga aatattttgg	180					
ctgacagacg ctccctttca aattaatgtt ttttgtccgc taggtcttgc gatgccacca	240					
aaagatcaga ttaaaaagtg gaaagaaaac ataccgttag ctaatcaagt aaatcaattc	300					

acatctgtac	aagaagagtg	ggatgacttc	tatcaaaaaa	ttgatcta	tttaaaaatac	360
aaggtaagg	cttgctcatt	cacttttgc	ctgcgcctg	aagacgcagt	aaaggagcta	420
aaaaccgcgt	gatgctgttt	aataggaacc	gttcaacag	tagaagaagc	attgtatgt	480
gaagaacggg	gaatggatat	agtagtcctt	caaggaaatg	aagccgggtgg	acatcgccga	540
gcattttac	cttccaaagg	tgaatctgc	gtatgtttaa	tggctctgtat	tccacaagca	600
gcagatgcac	tgagcgtacc	tgtcatatgc	gctggggaa	tgatagacca	cagaggagta	660
aaagcagctt	taaccctcg	agccaaaggc	gttcaaatcg	gttctgcctt	tttaatttgt	720
cacgagagta	acgcacatcc	agtgcataaa	cagaaaaatac	tagaagcaaa	cgaaggacat	780
acaaagctt	cgacattatt	ttcaggtaaa	gaggccagag	gaatcgtaaa	taaatggatg	840
gaagaaaaatg	aacagtttg	gacacaaacc	cttccgtacc	cttataaaaa	tacactaacy	900
aaggcaatga	gacagaaggc	ttcacttcaa	aataaccatg	atcagatgtc	tttatgggc	960
ggtcaaggga	tacggtcatt	gactgaggaa	atttcggtt	agcagcttt	aaatcagctt	1020
tgccaagagg	atataaaaat	atag				1044

<210> 22
 <211> 347
 <212> PRT
 <213> Bacillus subtilis
 <400> 22

Met	Asn	Glu	Phe	Met	Lys	Lys	Phe	Ser	Leu	Thr	Lys	Pro	Ile	Ile	Gln
1				5					10				15		

Ala	Pro	Met	Ala	Gly	Gly	Ile	Thr	Lys	Pro	Arg	Leu	Ala	Ser	Ala	Val
						20		25				30			

Ser	Asn	Gln	Gly	Ala	Leu	Gly	Ser	Leu	Ala	Ser	Gly	Tyr	Leu	Thr	Pro
		35					40				45				

Asp	Leu	Leu	Glu	Gln	Gln	Ile	Lys	Glu	Ile	Phe	Glu	Leu	Thr	Asp	Ala
		50				55			60						

Pro	Phe	Gln	Ile	Asn	Val	Phe	Val	Pro	Leu	Gly	Leu	Glu	Met	Pro	Pro
65					70				75				80		

Lys	Asp	Gln	Ile	Lys	Lys	Trp	Lys	Glu	Asn	Ile	Pro	Leu	Ala	Asn	Gln
				85				90				95			

Val	Asn	Gln	Phe	Thr	Ser	Val	Gln	Glu	Glu	Trp	Asp	Asp	Phe	Tyr	Gln
				100					105			110			

Lys Ile Asp Leu Ile Leu Lys Tyr Lys Val Lys Ala Cys Ser Phe Thr
 115 120 125
 Phe Asp Leu Pro Pro Glu Asp Ala Val Lys Glu Leu Lys Thr Ala Gly
 130 135 140
 Cys Cys Leu Ile Gly Thr Ala Ser Thr Val Glu Glu Ala Leu Leu Met
 145 150 155 160
 Glu Glu Arg Gly Met Asp Ile Val Val Leu Gln Gly Ser Glu Ala Gly
 165 170 175
 Gly His Arg Gly Ala Phe Leu Pro Ser Lys Gly Glu Ser Ala Val Gly
 180 185 190
 Leu Met Ala Leu Ile Pro Gln Ala Ala Asp Ala Leu Ser Val Pro Val
 195 200 205
 Ile Ala Ala Gly Gly Met Ile Asp His Arg Gly Val Lys Ala Ala Leu
 210 215 220
 Thr Leu Gly Ala Gln Gly Val Gln Ile Gly Ser Ala Phe Leu Ile Cys
 225 230 235 240
 His Glu Ser Asn Ala His Pro Val His Lys Gln Lys Ile Leu Glu Ala
 245 250 255
 Asn Glu Ala Asp Thr Lys Leu Thr Leu Phe Ser Gly Lys Glu Ala
 260 265 270
 Arg Gly Ile Val Asn Lys Trp Met Glu Glu Asn Glu Gln Phe Glu Thr
 275 280 285
 Gln Thr Leu Pro Tyr Pro Tyr Gln Asn Thr Leu Thr Lys Ala Met Arg
 290 295 300
 Gln Lys Ala Ser Leu Gln Asn Asn His Asp Gln Met Ser Leu Trp Ala
 305 310 315 320
 Gly Gln Gly Ile Arg Ser Leu Thr Glu Glu Ile Ser Val Lys Gln Leu
 325 330 335
 Leu Asn Gln Leu Cys Gln Glu Asp Ile Lys Ile
 340 345

<210> 23
 <211> 1128
 <212> DNA
 <213> Mycobacterium tuberculosis rv1533

 <400> 23
 atgcggacca gagtcgcccga gctgtcggtt gctgagtttc caaatatgcgc gttcagccac 60
 tgccggatg tgggtggccgc gggtgtccaaat gcgggccgggt tcgggatccct cgggtggcc 120
 gcacataggc ccaaacaaggct ggagagccggat ctgacaccttga tcgaggagca cacgggtggc 180
 aaggccgtacg gagtcgacgt gctgtcgccg cccaaataca tcggccggca gcaaggccgg 240
 atcgatggcc accggccggcc ggaggtcata cccgaagggc atcgcacctt cgtcgacgac 300
 ttgtcggttc gctatggcat ccccgccggc accggccggc agcgatcgat ctcggccgggt 360
 gggctgcaca tctcgcccaa gggttatcg ccgttgcgtt atgtggccct cgcccatgac 420
 atcccggtta tccgcacgcg gctcgccggc ccgcacccgg atctcgatggc gcgccggccac 480
 aaccatgacg tgctgggttc cgccttagcc ggcacggccg agcacccggc ggcacacccgg 540
 gctcgccgggtt ttgacactgtat cgtcgccggc ggcacccggagg ccggaggccca caccggccgg 600
 gtggcgacca tgggttcgtt tcccgaaagtc gtcgatgcgg tgcgtccaaac gccgggtcg 660
 gcccgccggc ggatcgcccg tggccggcccg atcgatgcgg cgttggccctt gggggccggaa 720
 ggccgtcggtt gccgggtcggtt ctgggttgc accgaaagaag ccgaaacggcc cccgggtggc 780
 aaggacaagt ttctggccgc aacatctcg gacacgggtgc ggtccggcgc gctaaccggc 840
 aaggccggccg gcatgtcgccg caccggctgg accgacgaat gggatcgccg tgacagcccc 900
 gaccggccgtt gcatgtcgccgtt gcaaggccggcctt ctgggtcgccg accccggcgtt ggcacatcaac 960
 caggccggccg gcaaggccggc ggcacccggcgtt gcatgtcgccg accccggcgtt ggcacatcaac 1020
 gtcgtcggtt cactcgccggc ggtgcgggtcg gcccgtcggtt tggtgttgc catgggtcg 1080
 gagttcatcg acaccgtcgcc gcaactgcag gggttgggttc aaagggtga 1128

<210> 24
 <211> 375
 <212> PRT
 <213> Mycobacterium tuberculosis rv1533

<400> 24

Met	Arg	Thr	Arg	Val	Ala	Glu	Leu	Leu	Gly	Ala	Glu	Phe	Pro	Ile	Cys
1															
				5				10						15	

Ala	Phe	Ser	His	Cys	Arg	Asp	Val	Val	Ala	Ala	Val	Ser	Asn	Ala	Gly
				20				25						30	

Gly Phe Gly Ile Leu Gly Ala Val Ala His Ser Pro Lys Arg Leu Glu

35	40	45
Ser Glu Leu Thr Trp Ile Glu Glu His Thr Gly Gly Lys Pro Tyr Gly		
50	55	60
Val Asp Val Leu Leu Pro Pro Lys Tyr Ile Gly Ala Glu Gln Gly Gly		
65	70	75
Ile Asp Ala Gln Gln Ala Arg Glu Leu Ile Pro Glu Gly His Arg Thr		
85	90	95
Phe Val Asp Asp Leu Leu Val Arg Tyr Gly Ile Pro Ala Val Thr Asp		
100	105	110
Arg Gln Arg Ser Ser Ser Ala Gly Gly Leu His Ile Ser Pro Lys Gly		
115	120	125
Tyr Gln Pro Leu Leu Asp Val Ala Phe Ala His Asp Ile Arg Leu Ile		
130	135	140
Ala Ser Ala Leu Gly Pro Pro Pro Pro Asp Leu Val Glu Arg Ala His		
145	150	155
Asn His Asp Val Leu Val Ala Ala Leu Ala Gly Thr Ala Gln His Ala		
165	170	175
Arg Arg His Ala Ala Ala Gly Val Asp Leu Ile Val Ala Gln Gly Thr		
180	185	190
Glu Ala Gly Gly His Thr Gly Glu Val Ala Thr Met Val Leu Val Pro		
195	200	205
Glu Val Val Asp Ala Val Ser Pro Thr Pro Val Leu Ala Ala Gly Gly		
210	215	220
Ile Ala Arg Gly Arg Gln Ile Ala Ala Ala Leu Ala Leu Gly Ala Glu		
225	230	235
Gly Val Trp Cys Gly Ser Val Trp Leu Thr Thr Glu Glu Ala Glu Thr		
245	250	255
Pro Pro Val Val Lys Asp Lys Phe Leu Ala Ala Thr Ser Ser Asp Thr		
260	265	270
Val Arg Ser Arg Ser Leu Thr Gly Lys Pro Ala Arg Met Leu Arg Thr		
275	280	285

Ala Trp Thr Asp Glu Trp Asp Arg Pro Asp Ser Pro Asp Pro Leu Gly
 290 295 300

; Met Pro Leu Gln Ser Ala Leu Val Ser Asp Pro Gln Leu Arg Ile Asn
 ; 305 310 315 320

Gln Ala Ala Gly Gln Pro Gly Ala Lys Ala Arg Glu Leu Ala Thr Tyr
 325 330 335

Phe Val Gly Gln Val Val Gly Ser Leu Asp Arg Val Arg Ser Ala Arg
 340 345 350

Ser Val Val Leu Asp Met Val Glu Glu Phe Ile Asp Thr Val Gly Gln
 355 360 365

Leu Gln Gly Leu Val Gln Arg
 370 375

<210> 25
<211> 1035
<212> DNA
<213> Mycobacterium tuberculosis rv2781c

<400> 25		
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ccggacgaccc cggcggttggc cgccggcggtg tccaaacgctg gccgggtttgg ttctgtcgcc	120	
ggcgccgtata tgagcgccgga cgggttcgccc gacgatatacg ccgtctgcgcg cgccggccact	180	
accgggtctta tcggagccaa tctgtttgtg ccccaaccca gcgctgcgcga ctggggccgcag	240	
ctggaggatt acgccccggc gctcgaagag gtgcgcgagt actaccacac cgagggtggcc	300	
cagcccgctt atgggtacgca cgacgactgg gtgcgcacaaac tccgagggttgc agccgtatgtt	360	
cgtccggagg tgggtgtgtt caccttcggc gcgcgcgcgc cggatgtctgt gcaggcggttg	420	
agcgccgtgg gactgtgtgtt ctgcgtatccc gtgcacgcgg tctacgaggcc cggatgttggcc	480	
attgcgcggc ggcggccacag cctgggtggtc caggggccggc ctgcggccgg gcacccgggaa	540	
acgttcgcgc cggacatggaa accccggtaacg gatgcgttc accaaacttctt cgtatcgatt	600	
ggcagcgcggc atgatgtgcg gctgggttgcg gccgggtggcc tggggcacggc tgaggacgtg	660	
gcccgcgtgc tgccggccgg agcgatcgcc ggcgcgggttgc gtaccgcatt gctgtggcc	720	
gacgaaggccgt gtaccaatgc cgacacccgt gccgcgtga agaatccaga gttcgtatggcc	780	
accctgggtca ctgcggccgtt ctgcgggttggc tatgcgcgcgg gtcgtggccaa caacttcact	840	
cgccctgtcg accacgtggc ggcgcgtgggt tatccggagg tccaccagat gacgaaaggccg	900	

atacggggcg ggccgggtgca ggcggacgac ccgcacggaa caaaccttg ggcgggatcg 960
 ggcacccgga agacccggcc gggacccgcg gccgacatca tcgcttcct tactccgac 1020
 gtgtgtcg cgtaa 1035

<210> 26
 <211> 344
 <212> PRT
 <213> Mycobacterium tuberculosis rv2781c

<400> 26

Met	Val	Leu	Gly	Phe	Trp	Asp	Ile	Ala	Val	Pro	Ile	Val	Gly	Ala	Pro
1				5					10				15		

Met Ala Gly Gly Pro Ser Thr Pro Ala Leu Ala Ala Ala Val Ser Asn
 20 25 30

Ala Gly Gly Leu Gly Phe Val Ala Gly Gly Tyr Leu Ser Ala Asp Arg
 35 40 45

Leu Ala Asp Asp Ile Ala Ala Ala Arg Ala Ala Thr Thr Gly Pro Ile
 50 55 60

Gly Ala Asn Leu Phe Val Pro Gln Pro Ser Val Ala Asp Trp Ala Gln
 65 70 75 80

Leu Glu Tyr Tyr Ala Asp Glu Leu Glu Glu Val Ala Glu Tyr Tyr His
 85 90 95

Thr Glu Val Gly Gln Pro Val Tyr Gly Asp Asp Asp Asp Trp Val Arg
 100 105 110

Lys Leu Glu Val Val Ala Asp Val Arg Pro Glu Val Val Ser Phe Thr
 115 120 125

Phe Gly Ala Pro Pro Asp Val Val Gln Arg Leu Ser Ala Leu Gly
 130 135 140

Leu Leu Val Ser Ile Thr Val Thr Ser Val Tyr Glu Ala Gly Val Ala
 145 150 155 160

Ile Ala Ala Gly Ala Asp Ser Leu Val Val Gln Gly Pro Ala Ala Gly
 165 170 175

Gly His Arg Gly Thr Phe Ala Pro Asp Met Glu Pro Gly Thr Glu Ser
 180 185 190

Leu His Gln Leu Leu Asp Arg Ile Gly Ser Ala His Asp Val Pro Leu
195 200 205

: Val Ala Ala Gly Gly Leu Gly Thr Ala Glu Asp Val Ala Ala Val Leu
: 210 215 220

Arg Arg Gly Ala Ile Ala Ala Gln Val Gly Thr Ala Leu Leu Leu Ala
225 230 235 240

Asp Glu Ala Gly Thr Asn Ala Ala His Arg Ala Ala Leu Lys Asn Pro
245 250 255

Glu Phe Asp Ala Thr Leu Val Thr Arg Ala Phe Ser Gly Arg Tyr Ala
260 265 270

Arg Gly Leu Ala Asn Asn Phe Thr Arg Leu Leu Asp His Val Ala Pro
275 280 285

Leu Gly Tyr Pro Glu Val His Gln Met Thr Lys Pro Ile Arg Ala Ala
290 295 300

Ala Val Gln Ala Asp Asp Pro His Gly Thr Asn Leu Trp Ala Gly Ser
 305 310 315 320

Ala His Arg Lys Thr Arg Pro Gly Pro Ala Ala Asp Ile Ile Ala Ser
325 330 335

Leu Thr Pro Asp Val Cys Ser Ala
340

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<210> 27
<211> 1068
<212> DNA
<213> Mycobacterium tuberculosis rv3553
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<400> 27 atgaggcgtgc gtacggccgt gaccggagctc atccggcatcg agcacccgggt ggtcgacgacc 60  
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ggcatactttgg cctcgccgacac catgacgctg gacgagctgg cggcgccgat cacaaaaggtc 180  
aaggccgtca ccggacaaggcc attccggggtg aacatcccgccg ccggacgcccggc cgacgcgggc 240  
gaccgcgtcg agttgtatgtat ccgcgggggggtt gtcggccggatgg cctctgttcgcg ttggccaccc 300  
aaacacggcgc tgatcgccgg gctcaaaggaa gccggccggccg tggtcataacc gtccatggcc 360  
ggggccaaac atgcgcgcacat ggtggccggcc tggggccggccg acggatgtat cgtcgacggcc 420
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ggcgaggggcg gcggccacac cggggccggtc gcccaccacgc tgctgttgcc gtcgggtgtc 480
 gaccccggtgg cgggcacccgg catcccggtg atcgcggccgg ggggtttttt cgacggggcgc 540
 gggcttagccg cggcggttgtg ctacggcgcc gccccgggtgg ccatgggcac ccggtttctg 600
 ctacacctgg attccacccgt gcccacacgc gtcaaacacgc gttacactgtca ggccgggttg 660
 gacccgcaccc tggtcacccac ccgcgtcgac gggatggccgc accgggtgtc ggcacccgg 720
 ctggtcgaga agctggaaag cggctcgccg gcacgagggt tcgcggccgc gctgcgcaat 780
 gccggcaagt ttagacggat gtcgcagatg acctggcggtt cgatgatccg agacggcttg 840
 accatgcgcc acggcaagga attgacctgg tcacagggtc tgatggccgc aaacaccccg 900
 atgtctgtca aaggccggct ggtcgacccgc aacacccgggg ccgggggtgtc ggcacccggc 960
 caggtagegg gcattcttga cgacacttccgt tcgtgcaaaag agctgatcga gtcgatctgt 1020
 cttgacgcca tcacacatcc acaaaccgcata tctggcgtgg tggagtgta 1068

<211> 28
 <211> 355
 <212> PRT
 <213> Mycobacterium tuberculosis rv3553

<400> 28

Met	Arg	Leu	Arg	Thr	Pro	Leu	Thr	Glu	Leu	Ile	Gly	Ile	Glu	His	Pro
1						5				10			15		

Val	Val	Gln	Thr	Gly	Met	Gly	Trp	Val	Ala	Gly	Ala	Arg	Leu	Val	Ser
					20				25			30			

Ala	Thr	Ala	Asn	Ala	Gly	Gly	Leu	Gly	Ile	Leu	Ala	Ser	Ala	Thr	Met
					35			40				45			

Thr	Leu	Asp	Glu	Leu	Ala	Ala	Ile	Thr	Lys	Val	Lys	Ala	Val	Thr
50						55			60					

Asp	Lys	Pro	Phe	Gly	Val	Asn	Ile	Arg	Ala	Asp	Ala	Ala	Asp	Ala	Gly
65					70				75			80			

Asp	Arg	Val	Glu	Leu	Met	Ile	Arg	Glu	Gly	Val	Arg	Val	Ala	Ser	Phe
					85			90			95				

Ala	Leu	Ala	Pro	Lys	Gln	Gln	Leu	Ile	Ala	Arg	Leu	Lys	Glu	Ala	Gly
					100				105			110			

Ala	Val	Val	Ile	Pro	Ser	Ile	Gly	Ala	Ala	Lys	His	Ala	Arg	Lys	Val
					115				120			125			

Ala Ala Trp Gly Ala Asp Ala Met Ile Val Gln Gly Gly Glu Gly
 130 135 140

Gly His Thr Gly Pro Val Ala Thr Thr Leu Leu Leu Pro Ser Val Leu
 145 150 155 160

Asp Ala Val Ala Gly Thr Gly Ile Pro Val Ile Ala Ala Gly Gly Phe
 165 170 175

Phe Asp Gly Arg Gly Leu Ala Ala Leu Cys Tyr Gly Ala Ala Gly
 180 185 190

Val Ala Met Gly Thr Arg Phe Leu Leu Thr Ser Asp Ser Thr Val Pro
 195 200 205

Asp Ala Val Lys Arg Arg Tyr Leu Gln Ala Gly Leu Asp Gly Thr Val
 210 215 220

Val Thr Thr Arg Val Asp Gly Met Pro His Arg Val Leu Arg Thr Glu
 225 230 235 240

Leu Val Glu Lys Leu Glu Ser Gly Ser Arg Ala Arg Gly Phe Ala Ala
 245 250 255

Ala Leu Arg Asn Ala Gly Lys Phe Arg Arg Met Ser Gln Met Thr Trp
 260 265 270

Arg Ser Met Ile Arg Asp Gly Leu Thr Met Arg His Gly Lys Glu Leu
 275 280 285

Thr Trp Ser Gln Val Leu Met Ala Ala Asn Thr Pro Met Leu Leu Lys
 290 295 300

Ala Gly Leu Val Asp Gly Asn Thr Glu Ala Gly Val Leu Ala Ser Gly
 305 310 315 320

Gln Val Ala Gly Ile Leu Asp Asp Leu Pro Ser Cys Lys Glu Leu Ile
 325 330 335

Glu Ser Ile Val Leu Asp Ala Ile Thr His Leu Gln Thr Ala Ser Ala
 340 345 350

Leu Val Glu
 355

<210> 29
 <211> 969
 <212> DNA
 <213> Mycobacterium tuberculosis rv0021c

<400> 29
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 ggccatcgatcg gggccggcta tggggaccgg gattgggtgg cccggcagtt cgatctcgcc 180
 gctggagcgc cgggtggctg cgggttcata accttggcttt tggcccgcca accgcagctg 240
 ctgcacctcg cgctgcagta tgagccggtg gccgtgtatgc tgcgttgg ggaccccgcc 300
 gtttcgctg acgccatcaa gtccgcccga acgcgggtgg tctgcgcagat caaaaaccgg 360
 acccaggccg akgcggccct gcaggatcgcc gccgatgtgt tgggtggctca gggcaccgg 420
 gccgggtggcc acggggccagg tccacgttcc accctgaccc tggtaaccgaa aatcgctgac 480
 ctggtcaccc cgccggggaa tgatatccccg tgcgtccgg ccggggcat cgccgcggc 540
 cggggcccttgc cggccgcgtt gatgtgggc gccgcgggg tattggtgg tgcgcgttcc 600
 tacgcccacgg tgcggcgtt atccacaccc caggcgcggg accccgtgtc ggcggccact 660
 ggcgacgaca tggccgcac cactatctac gatcgactac ggcgcgtatcc ctggccgcaa 720
 ggacacacga tgaggcgtgt aagcaacgc ctcaccgcatt aattcgagga caccgaactc 780
 gagacattcc atcgcaaga agccatggcc agatattggc gaggcgttgc tgcgtgtac 840
 tacagcatcg ccaatgtcac cgccggctaa gccgcggggcc tggtaatgc cgtccctgc 900
 ggcggcgaacg tgataacccg tatggcgc aaagcggcga ggacgtgtac cgcgatgc 960
 ggccgtgtaa 969

<210> 30
 <211> 322
 <212> PRT
 <213> Mycobacterium tuberculosis rv0021c

<400> 30

Met	Val	Leu	Ser	Thr	Ala	Phe	Ser	Gln	Met	Phe	Gly	Ile	Asp	Tyr	Pro
1									5					10	

Ile	Val	Ser	Ala	Pro	Met	Asp	Leu	Ile	Ala	Gly	Gly	Glu	Leu	Ala	Ala
								20				25		30	

Ala	Val	Ser	Gly	Ala	Gly	Gly	Leu	Gly	Ile	Gly	Gly	Tyr	Gly	
35									40			45		

Asp Arg Asp Trp Leu Ala Arg Gln Phe Asp Leu Ala Ala Gly Ala Pro
 50 55 60

Val Gly Cys Gly Phe Ile Thr Trp Ser Leu Ala Arg Gln Pro Gln Leu
 65 70 75 80

Leu Asp Leu Ala Leu Gln Tyr Glu Pro Val Ala Val Met Leu Ser Phe
 85 90 95

Gly Asp Pro Ala Val Phe Ala Asp Ala Ile Lys Ser Ala Gly Thr Arg
 100 105 110

Leu Val Cys Gln Ile Gln Asn Arg Thr Gln Ala Glu Arg Ala Leu Gln
 115 120 125

Val Gly Ala Asp Val Leu Val Ala Gln Gly Thr Glu Ala Gly Gly His
 130 135 140

Gly His Gly Pro Arg Ser Thr Leu Thr Leu Val Pro Glu Ile Val Asp
 145 150 155 160

Leu Val Thr Ala Arg Gly Thr Asp Ile Pro Val Ile Ala Ala Gly Gly
 165 170 175

Ile Ala Asp Gly Arg Gly Leu Ala Ala Ala Leu Met Leu Gly Ala Ala
 180 185 190

Gly Val Leu Val Gly Thr Arg Phe Tyr Ala Thr Val Glu Ala Leu Ser
 195 200 205

Thr Pro Gln Ala Arg Asp Pro Leu Leu Ala Ala Thr Gly Asp Asp Met
 210 215 220

Cys Arg Thr Thr Ile Tyr Asp Gln Leu Arg Arg Tyr Pro Trp Pro Gln
 225 230 235 240

Gly His Thr Met Ser Val Leu Ser Asn Ala Leu Thr Asp Gln Phe Glu
 245 250 255

Asp Thr Glu Leu Asp Ile Leu His Arg Glu Glu Ala Met Ala Arg Tyr
 260 265 270

Trp Arg Ala Val Ala Ala Arg Asp Tyr Ser Ile Ala Asn Val Thr Ala
 275 280 285

Gly Gln Ala Ala Gly Leu Val Asn Ala Val Leu Pro Ala Ala Asp Val

290

295

300

Ile Thr Gly Met Ala Gln Gln Ala Ala Arg Thr Leu Thr Ala Met Arg
 305 310 315 320

Ala Val

<210> 31
<211> 1131
<212> DNA
<213> Mycobacterium tuberculosis rv1894c

<400> 31		
atgcacactg ccatttgcgca cgagctcggt atcgagtttc ctatTTTC cttcaactac	60	
tggccgcatg tgggtggtcgc cgtcagcaaa gctgggtggtt ttgggtgtct cggagcagg	120	
gggttcacgcc cggagcagct ggagatcgag ctcaactggaa tocatgaaaca catcgccgac	180	
cacccttaacg gggtcgacat cgtatcccc aacaagtacg agggcatggaa ctcccagctg	240	
tccggcgatg agctcgccaa gacgctcggt tcgatggtcc cgcaggagca tctggacttc	300	
gcccccaaga tcctcgccga tcatgggttc cccgtcgagg acgcccacgaa ggacagctg	360	
cagctgtcg gttggaccga ggcgacggcc accccacagg tegacgoggc gctgaagcac	420	
cccaagatga cgatggtcgc caacgcgtt ggcacccccc cagcgacat gatcaagcac	480	
atccacgact cgggtcgcaa ggtggccgca ttgtggcgct caccctcgca ggcggccgaa	540	
cacggccatg cggggcgtcgaa catcatcgtc gcccaggggc gcgaggccgg cggggactgt	600	
ggcgaggatgg gtcatttgt gttgtggctt caggtcgctca aggaggatgc gccgggtccg	660	
gtgttggcggtt cgggtggcat cggcagcggt cagcagatcg ctgcagcggtt ggcgttgggg	720	
acccaaagggg catggacggg ttgcagttt ctgtatggcg aggaagccgc aaacacccgc	780	
gttcaacagg cgcatacgat caaggcgacc agccgcgaca ccgtgcgcag tcgttccctc	840	
acgggtaaggc cggcccgat gtcgcgcaac gactggactg aggctggaa gcaacccggag	900	
agcccgaaaggc cgctcggtat gccgtcgaa tacatggctt cccgtcgcc cgtcaaaaggc	960	
acacataaat acccgaaacgaa gaccgtcgac gtcgcgttca acccggtgggg gcagggttgc	1020	
gggcagttca ccaagggtggaa aaagacggctt accgttatacg aacgtgggttgc gcaaggatgc	1080	
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<210> 32
<211> 376
<212> PRT
<213> Mycobacterium tuberculosis rv1894c

<400> 32

Met His Thr Ala Ile Cys Asp Glu Leu Gly Ile Glu Phe Pro Ile Phe			
1	5	10	15

Ala Phe Thr His Cys Arg Asp Val Val Val Ala Val Ser Lys Ala Gly		
20	25	30

Gly Phe Gly Val Leu Gly Ala Val Gly Phe Thr Pro Glu Gln Leu Glu		
35	40	45

Ile Glu Leu Asn Trp Ile Asp Glu His Ile Gly Asp His Pro Tyr Gly		
50	55	60

Val Asp Ile Val Ile Pro Asn Lys Tyr Glu Gly Met Asp Ser Gln Leu			
65	70	75	80

Ser Ala Asp Glu Leu Ala Lys Thr Leu Arg Ser Met Val Pro Gln Glu		
85	90	95

His Leu Asp Phe Ala Arg Lys Ile Leu Ala Asp His Gly Val Pro Val		
100	105	110

Glu Asp Ala Asp Glu Asp Ser Leu Gln Leu Leu Gly Trp Thr Glu Ala		
115	120	125

Thr Ala Thr Pro Gln Val Asp Ala Ala Leu Lys His Pro Lys Met Thr		
130	135	140

Met Val Ala Asn Ala Leu Gly Thr Pro Pro Ala Asp Met Ile Lys His			
145	150	155	160

Ile His Asp Ser Gly Arg Lys Val Ala Ala Leu Cys Gly Ser Pro Ser		
165	170	175

Gln Ala Arg Lys His Ala Asp Ala Gly Val Asp Ile Ile Ile Ala Gln		
180	185	190

Gly Gly Glu Ala Gly Gly His Cys Gly Glu Val Gly Ser Ile Val Leu		
195	200	205

Trp Pro Gln Val Val Lys Glu Val Ala Pro Val Pro Val Leu Ala Ala		
210	215	220

Gly Gly Ile Gly Ser Gly Gln Gln Ile Ala Ala Leu Ala Leu Gly			
225	230	235	240

Thr Gln Gly Ala Trp Thr Gly Ser Gln Trp Leu Met Val Glu Glu Ala
 245 250 255

Ala Asn Thr Ala Val Gln Gln Ala Ala Tyr Val Lys Ala Thr Ser Arg
 260 265 270

Asp Thr Val Arg Ser Arg Ser Phe Thr Gly Lys Pro Ala Arg Met Leu
 275 280 285

Arg Asn Asp Trp Thr Glu Ala Trp Glu Gln Pro Glu Ser Pro Lys Pro
 290 295 300

Leu Gly Met Pro Leu Gln Tyr Met Val Ser Gly Met Ala Val Lys Ala
 305 310 315 320

Thr His Lys Tyr Pro Asn Glu Thr Val Asp Val Ala Phe Asn Pro Val
 325 330 335

Gly Gln Val Val Gly Gln Phe Thr Lys Val Glu Lys Thr Ala Thr Val
 340 345 350

Ile Glu Arg Trp Val Gln Glu Tyr Leu Glu Ala Thr Ala Arg Leu Asp
 355 360 365

Ala Leu Asn Ala Ala Ala Ser Val
 370 375

<210> 33
 <211> 945
 <212> DNA
 <213> Thermotoga maritima

<400> 33					
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ggaaatcatcg gatccggagc catgaagccg gacgacctga gaaaaggcgat ctccgaactc					180
agacagaaga cggacaaacc cttecggtta aacataatcc ttgtctctcc gtggggccgac					240
gatctcgta aggttgtcat agaagagaaa gtaccgtcg tcacgttcgg tgcccccaaac					300
ccaacgaagt acataaggaa actcaaggaa aacggAACaa aggtgtatcc cggtgtcgcc					360
tccgactctc tggcaaggat ggtggaaaga gccccggccggtat agcggaaagg					420
atggagtccg gtggcacat aggtgaagtc acaacccctcg ttctcgtaa caaagtctcc					480
aggagtgtga acatccccgt gatcgacgcg ggaggcatcg ccgacggaaag aggtatggca					540

gccgccttcg cactcggagc ggaagccgtt cagatggaa ccaggttgt ggcgagtgtg 600
 gaaagcgacg tgccacccggt ttacaaaagaa aagatcgtca aggcttccat aagagacacc 660
 gttgtgacgg gagccaaact tggacacccc gcgcgcgttc tcagaactcc ctttcaagg 720
 aagatccagg agatggagtt tgaaaacccc atgcaggctg aagaatgct ggtggaaagt 780
 ctcaagaagag cggtcggtga aggcgatctg gagagaggat ctttcattgtt gggacagagc 840
 gccggcttga tcgatgagat aaaacccgtt aagcagatca tagaggatata ccttgaaggag 900
 ttcaaaagaaa cggtggagaa gctgaggggg tacatcgaag agtga 945

<211> 34
 <211> 314
 <212> PRT
 <213> Thermotoga maritima

<400> 34

Met	Thr	Val	Arg	Thr	Arg	Val	Thr	Asp	Leu	Leu	Glu	Ile	Glu	His	Pro
1									5			10			15

Ile	Leu	Met	Gly	Gly	Met	Ala	Trp	Ala	Gly	Thr	Pro	Thr	Leu	Ala	Ala
		20							25				30		

Ala	Val	Ser	Glu	Ala	Gly	Gly	Leu	Gly	Ile	Ile	Gly	Ser	Gly	Ala	Met
							35				40			45	

Lys	Pro	Asp	Asp	Leu	Arg	Lys	Ala	Ile	Ser	Glu	Leu	Arg	Gln	Lys	Thr
						50				55			60		

Asp	Lys	Pro	Phe	Gly	Val	Asn	Ile	Ile	Leu	Val	Ser	Pro	Trp	Ala	Asp
65							70				75			80	

Asp	Leu	Val	Lys	Val	Cys	Ile	Glu	Glu	Lys	Val	Pro	Val	Val	Thr	Phe
						85			90				95		

Gly	Ala	Gly	Asn	Pro	Thr	Lys	Tyr	Ile	Arg	Glu	Leu	Lys	Glu	Asn	Gly
						100			105			110			

Thr	Lys	Val	Ile	Pro	Val	Val	Ala	Ser	Asp	Ser	Leu	Ala	Arg	Met	Val
							115				120		125		

Glu	Arg	Ala	Gly	Ala	Asp	Ala	Val	Ile	Ala	Glu	Gly	Met	Glu	Ser	Gly
							130			135		140			

Gly	His	Ile	Gly	Glu	Val	Thr	Thr	Phe	Val	Leu	Val	Asn	Lys	Val	Ser
145								150			155		160		

Arg Ser Val Asn Ile Pro Val Ile Ala Ala Gly Gly Ile Ala Asp Gly
 165 170 175

Arg Gly Met Ala Ala Ala Phe Ala Leu Gly Ala Glu Ala Val Gln Met
 180 185 190

Gly Thr Arg Phe Val Ala Ser Val Glu Ser Asp Val His Pro Val Tyr
 195 200 205

Lys Glu Lys Ile Val Lys Ala Ser Ile Arg Asp Thr Val Val Thr Gly
 210 215 220

Ala Lys Leu Gly His Pro Ala Arg Val Leu Arg Thr Pro Phe Ala Arg
 225 230 235 240

Lys Ile Gln Glu Met Glu Phe Glu Asn Pro Met Gln Ala Glu Glu Met
 245 250 255

Leu Val Gly Ser Leu Arg Arg Ala Val Val Glu Gly Asp Leu Glu Arg
 260 265 270

Gly Ser Phe Met Val Gly Gln Ser Ala Gly Leu Ile Asp Glu Ile Lys
 275 280 285

Pro Val Lys Gln Ile Ile Glu Asp Ile Leu Lys Glu Phe Lys Glu Thr
 290 295 300

Val Glu Lys Leu Arg Gly Tyr Ile Glu Glu
 305 310

<210> 35
 <211> 1092
 <212> DNA
 <213> Helicobacter pylori

<400> 35
 atggtatcaa cactcaaacc gctaaaaatc ggtaaacaca ccataaaatt ccctatttt 60
 caagggggca tgggtgtggg gattagctgg gatgaactag ctggaaatgt tgccaaagaa 120
 gggcttttag gagtgatttc agccgtaggg actggttatt ataaaaacat ggcgtttgt 180
 gaaaggattt tggctaaaaa accctttgaa gccttgaatt ttactccaa aaaagcggtt 240
 aatgagattt ttgcaaacgc tagaaaatt tgccggaaaca agcctttggg ggcgaatatt 300
 ttatacgcta tcaatgacta tggccgtgtt ttaaggact cttgtgaggc gggggcgaat 360
 attatcatta caggggctgg tttgcccaact aacatgcctaa ggatttttagc 420

gatgtggcgc tcatccatat catttcctca gogaaggctt taaaaatcct ttgtaaaaaga	480
tggagcgatc gctataaaag aatcccgac gcattcattg tggaaaggcc tttgagtggg	540
gggcattcagg gctttaata cgaagatgtt tc当地aaagaag aattccaatt agaaaaactta	600
gtgcctaaag tcgttggaaagc ttcttaagaa tgccccata tccctatcat cgccgcgggg	660
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atggcgactc gtttttagg cacaaaagaa tgcgcgcta aagcgatgc cgatctttg	780
cccacgctca aaaaagaaga tattttactc atcaaatcgc ctgttaggcta tccggctagg	840
gctatcaata cgggggtat caaacgcatt gaagaggta acgcgcctaa aatcgcatgc	900
gtgaccaatt gtgtacgc ttgttaacagg ggtgaagaag ctaaaaaggt gggctattgt	960
atcgctgatc gttttggggcg cagttatcta ggaaacagag aagagggct ttatttacc	1020
ggggctaatg gctatagatg ggataagatt atcagcgtgc atgaattgtat taaagagctt	1080
acagagggtt aa	1092

<210> 36
<211> 363
<212> PRT
<213> Helicobacter pylori

<400> 36

Met Val Ser Thr Leu Lys Pro Leu Lys Ile Gly Lys His Thr Ile Lys			
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Phe Pro Ile Phe Gln Gly Gly Met Gly Val Gly Ile Ser Trp Asp Glu			
20	25	30	

Leu Ala Gly Asn Val Ala Lys Glu Gly Ala Leu Gly Val Ile Ser Ala			
35	40	45	

Val Gly Thr Gly Tyr Tyr Lys Asn Met Arg Phe Val Glu Arg Ile Val			
50	55	60	

Ala Lys Lys Pro Phe Glu Ala Leu Asn Phe Tyr Ser Lys Lys Ala Leu			
65	70	75	80

Asn Glu Ile Phe Ala Asn Ala Arg Lys Ile Cys Gly Asn Lys Pro Leu			
85	90	95	

Gly Ala Asn Ile Leu Tyr Ala Ile Asn Asp Tyr Gly Arg Val Leu Arg			
100	105	110	

Asp Ser Cys Glu Ala Gly Ala Asn Ile Ile Ile Thr Gly Ala Gly Leu

115	120	125
Pro Thr Asn Met Pro Glu Phe Ala Lys Asp Phe Ser Asp Val Ala Leu		
130	135	140
Ile Pro Ile Ile Ser Ser Ala Lys Ala Leu Lys Ile Leu Cys Lys Arg		
145	150	155
Trp Ser Asp Arg Tyr Lys Arg Ile Pro Asp Ala Phe Ile Val Glu Gly		
165	170	175
Pro Leu Ser Gly Gly His Gln Gly Phe Lys Tyr Glu Asp Cys Phe Lys		
180	185	190
Glu Glu Phe Gln Leu Glu Asn Leu Val Pro Lys Val Val Glu Ala Ser		
195	200	205
Lys Glu Trp Gly Asn Ile Pro Ile Ile Ala Ala Gly Gly Ile Trp Asp		
210	215	220
Lys Lys Asp Ile Asp Thr Met Leu Ser Leu Gly Ala Ser Gly Val Gln		
225	230	235
Met Ala Thr Arg Phe Leu Gly Thr Lys Glu Cys Asp Ala Lys Ala Tyr		
245	250	255
Ala Asp Leu Leu Pro Thr Leu Lys Lys Glu Asp Ile Leu Leu Ile Lys		
260	265	270
Ser Pro Val Gly Tyr Pro Ala Arg Ala Ile Asn Thr Gly Val Ile Lys		
275	280	285
Arg Ile Glu Glu Gly Asn Ala Pro Lys Ile Ala Cys Val Ser Asn Cys		
290	295	300
Val Ala Pro Cys Asn Arg Gly Glu Ala Lys Lys Val Gly Tyr Cys		
305	310	315
Ile Ala Asp Gly Leu Gly Arg Ser Tyr Leu Gly Asn Arg Glu Glu Gly		
325	330	335
Leu Tyr Phe Thr Gly Ala Asn Gly Tyr Arg Val Asp Lys Ile Ile Ser		
340	345	350
Val His Glu Leu Ile Lys Glu Leu Thr Glu Gly		
355	360	

<210> 37
 <211> 825
 <212> DNA
 <213> Archaeoglobus fulgidus

<400> 37
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 gcttcgcgc gcctttgcgc tgaaaaacta aaagaggaga tagagaaaatgtaaacaagg 180
 actgataaagc cttcgcgcgt gaacattcca atatatcgc cccgctcgga gaagaatctt 240
 gagactgcac ttaaagctga tgttgggatt atttacacct ctgcaggaag cccggagaaa 300
 tacactgaga gagtaaaggaa atccggggca aaagtctatac acaagggtgtc gaggttgaaa 360
 gaggggctga aagccggaa ggcggggatgt gatgtctgtgg ttgcgtatggg ctttggggc 420
 ggagggatta tagggaggag tggtgttaaca tcctttctgt tatttctgtga gtttgcgcac 480
 aacctcgac ttccagtgt agccgctggc gggatagcag atgagaggggg atttgcgtca 540
 gcccgtattc tcggagcgga aggtgtttagt attggcacga gactgttgc aaccaaagag 600
 tgccttgcgc tgaaaggcat taagcaagct atttaaaag ccacctgcga ctccacatgt 660
 gtttattgaga gccccgttgt aatgagagct ctcaaggccag agctgagcgg agattctgt 720
 aatctctgttc tgggaggggca ggtttcaggg ctgattaagg agattttac ggttgaagag 780
 gtaatcagga aaattgcaga ggggctgaat aaagcttaat tctaa 825

<210> 38
 <211> 274
 <212> PRT
 <213> Archaeoglobus fulgidus

<400> 38
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 1 5 10 15

Gly	Pro	Met	Ala	Gly	Ile	Thr	Leu	Gly	Glu	Phe	Ala	Ser	Thr	Val	Ser
20								25						30	

Glu Ala Gly Gly Leu Gly Val Ile Ala Ser Ala Gly Leu Ser Pro Glu
 35 40 45

Lys	Leu	Lys	Glu	Glu	Ile	Glu	Lys	Val	Lys	Asn	Arg	Thr	Asp	Lys	Pro
50								55						60	

Phe Ala Val Asn Ile Pro Ile Tyr Gln Pro Gly Ser Glu Lys Asn Leu

42

65	70	75	80
Glu Thr Ala Leu Lys Ala Asp Val Gly Ile Ile Tyr Thr Ser Ala Gly			
85		90	95
Ser Pro Glu Lys Tyr Thr Glu Arg Val Lys Glu Ser Gly Ala Lys Val			
100		105	110
Ile His Lys Val Ser Arg Leu Lys Glu Gly Leu Lys Ala Glu Lys Ala			
115		120	125
Gly Val Asp Ala Val Val Ala Met Gly Phe Glu Ala Gly Gly Ile Ile			
130		135	140
Gly Arg Ser Gly Val Thr Ser Phe Cys Leu Ile Pro Glu Leu Ala Asp			
145		150	155
Asn Leu Ser Ile Pro Val Val Ala Ala Gly Gly Ile Ala Asp Glu Arg			
165		170	175
Gly Phe Ala Ala Ala Leu Ile Leu Gly Ala Glu Gly Val Glu Ile Gly			
180		185	190
Thr Arg Leu Leu Ala Thr Lys Glu Cys Pro Val Pro Glu Ser Ile Lys			
195		200	205
Gln Ala Ile Leu Lys Ala Thr Cys Asp Ser Thr Met Val Ile Glu Ser			
210		215	220
Pro Val Val Met Arg Ala Leu Lys Pro Glu Leu Ser Gly Asp Ser Glu			
225		230	235
Asn Pro Ala Leu Gly Gly Gln Val Ser Gly Leu Ile Lys Glu Ile Leu			
245		250	255
Thr Val Glu Val Ile Arg Lys Ile Ala Glu Gly Leu Asn Lys Ala			
260		265	270
Lys Phe			

<210> 39
<211> 1125
<212> DNA
<213> Williopsis saturnus
<400> 39

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atggttcga	tccctatggg	ctcgctgagt	gagaagtgt	atgcatttga	gacccttgt	180
gaaaattttg	atgaatttgt	tggtattct	ggaaggatag	tcaacttcaa	cttcttgc	240
cataaggagc	ctcggttccg	gagagctgtat	gtcaacgagg	aatggctcaa	gaagtatgac	300
aagatatacg	gcaaaacccg	aatttgcgttt	gacaaaagg	agctgaagtt	gttatatcca	360
tcttttagt	ccatgttgc	tccacaacat	ccgactgtgc	ggctactgaa	gaatctcaag	420
ccaaagatttgc	tcaagttcca	ctttgggtta	ccccatgagg	cggtgattga	atctctccag	480
gcaagcata	ttaagatctt	tgtcactgtc	acaaatctac	aggagttca	gcaggcttat	540
gagtcataat	tggatgggt	cgtccataa	ggatggaaag	ctggtgacat	tcgtggata	600
ttcaaggcttca	atgacgtcga	agatggacaa	ctgaagacgt	tggatctcgt	tagtactatt	660
gttatttaca	ttgactcgcc	tagtatctcc	aatccaccaat	ttatcattgc	acgcccgggt	720
attcatgtat	atgagtcatt	caaagaatttgc	cttcaattca	acatttgc	cgttcagttt	780
ggtaactgttt	ggttaccatc	gagccaggcc	acaatatctc	ctgaacattt	gaagatgtt	840
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gggcctcagt	actccgcatt	tcttgctgga	tcttaactatc	acaaatcttgc	gaaggatcgt	1080
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<210> 40
<211> 374
<212> PRT
<213> Williopsis saturnus

<400> 40

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20 25 30

Ala Thr Val Thr Arg Leu Gly Gly Ile Gly Ser Ile Pro Met Gly Ser
35 40 45

Leu Ser Glu Lys Cys Asp Ala Ile Glu Thr Gln Leu Glu Asn Phe Asp
50 55 60

Glu Leu Val Gly Asp Ser Gly Arg Ile Val Asn Leu Asn Phe Phe Ala
 65 70 75 80

His Lys Glu Pro Arg Ser Gly Arg Ala Asp Val Asn Glu Glu Trp Leu
 85 90 95

Lys Lys Tyr Asp Lys Ile Tyr Gly Lys Ala Gly Ile Glu Phe Asp Lys
 100 105 110

Lys Glu Leu Lys Leu Leu Tyr Pro Ser Phe Arg Ser Ile Val Asp Pro
 115 120 125

Gln His Pro Thr Val Arg Leu Leu Lys Asn Leu Lys Pro Lys Ile Val
 130 135 140

Ser Phe His Phe Gly Leu Pro His Glu Ala Val Ile Glu Ser Leu Gln
 145 150 155 160

Ala Ser Asp Ile Lys Ile Phe Val Thr Val Thr Asn Leu Gln Glu Phe
 165 170 175

Gln Gln Ala Tyr Glu Ser Lys Leu Asp Gly Val Val Leu Gln Gly Trp
 180 185 190

Glu Ala Gly Gly His Arg Gly Asn Phe Lys Ala Asn Asp Val Glu Asp
 195 200 205

Gly Gln Leu Lys Thr Leu Asp Leu Val Ser Thr Ile Val Asp Tyr Ile
 210 215 220

Asp Ser Ala Ser Ile Ser Asn Pro Pro Phe Ile Ile Ala Ala Gly Gly
 225 230 235 240

Ile His Asp Asp Glu Ser Ile Lys Glu Leu Leu Gln Phe Asn Ile Ala
 245 250 255

Ala Val Gln Leu Gly Thr Val Trp Leu Pro Ser Ser Gln Ala Thr Ile
 260 265 270

Ser Pro Glu His Leu Lys Met Phe Gln Ser Pro Lys Ser Asp Thr Met
 275 280 285

Met Thr Ala Ala Ile Ser Gly Arg Asn Leu Arg Thr Ile Ser Thr Pro
 290 295 300

Phe Leu Arg Asp Leu His Gln Ser Ser Pro Leu Ala Ser Ile Pro Asp
 305 310 315 320

Tyr Pro Leu Pro Tyr Asp Ser Phe Lys Ser Leu Ala Asn Asp Ala Lys
 325 330 335

Gln Ser Gly Lys Gly Pro Gln Tyr Ser Ala Phe Leu Ala Gly Ser Asn
 340 345 350

Tyr His Lys Ser Trp Lys Asp Thr Arg Ser Thr Glu Glu Ile Phe Ser
 355 360 365

Ile Leu Val Gln Asp Leu
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<210> 41
<211> 1215
<212> DNA
<213> *Saccharomyces cerevisiae*

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cctatggcgg gggtcacgc tattgaaatg gcccgcataagg ctgttattgc gggcgccata	240
gttctactac ccctatcccc ctttagacttc agaaaggctca atgatattga aaagcttaaa	300
ctgtatggttt cacaatttag agatacaagta gcccgtatc cttagaggg caatcttcaac	360
ctaaactttt ttggccatga tategttgat aaaccgacccg atcttcaaac agctaactgg	420
gcggaaacctat acagaaggct tatgtatgtg ccgtatgtata tgaatggat taaatttgtat	480
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tacccatccat atggcttttag gcctaaaatc attagttcc attttggcca tccgtcgaaa	600
tctacaatag aatatttaca aaaaatttggaa attctaaattt ttgtgactgc cacctctgtat	660
agagaaggatc gattgttagc acgtctccgc attaatggca tagtgtgtca aggctatgaa	720
gcggggggac atagaggaaa ttctcttagta aatgccccca aagatgtatc aaacttatca	780
actgtacaat ttgtgaaaag aacagtgtatc gaacttgcgt aaatgaaaaa taaaggcttt	840
atacatgtca ctccccctgt cattgcgcga ggtgttataa tggattccaa agatataatca	900
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gaatccaatg cataaaaaaaaa cttttcaagc cccttcaactc gagaaacaac aactaaaaatg	1020
gttaatataa tatcaggaaa gcctgcagg accatctcta ctccctttat cgaaaaaaatgc	1080
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caagtaagaa aaaagtatcc agaattggct aacttttatt tagctggaca aggatttcag 1140
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<210> 42
 <211> 404
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 42

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														10	15

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 20 25 30

Leu Arg Tyr Pro Ile Ile Gln Ala Pro Met Ala Gly Val Thr Thr Ile
 35 40 45

Glu Met Ala Ala Lys Ala Cys Ile Ala Gly Ala Ile Ala Ser Leu Pro
 50 55 60

Leu Ser His Leu Asp Phe Arg Lys Val Asn Asp Ile Glu Lys Leu Lys
 65 70 75 80

Leu Met Val Ser Gln Phe Arg Asp Gln Val Ala Asp Glu Ser Leu Glu
 85 90 95

Gly Asn Leu Asn Leu Asn Phe Phe Cys His Asp Ile Val Asp Lys Pro
 100 105 110

Thr Asp Leu Gln Thr Ala Asn Trp Ala Lys Leu Tyr Arg Lys Ser Met
 115 120 125

Asn Val Pro Ile Asp Met Asn Glu Ile Lys Phe Asp Asn Gly Asn Val
 130 135 140

Ser Phe Lys Ala Phe Glu Lys Glu Asn Ala Leu Gln Asp Phe Phe Gln
 145 150 155 160

Tyr Leu Ser Asp Gly Phe Arg Pro Lys Ile Ile Ser Phe His Phe Gly
 165 170 175

His Pro Ser Lys Ser Thr Ile Glu Tyr Leu Gln Lys Ile Gly Ile Leu
 180 185 190

Ile Phe Val Thr Ala Thr Ser Val Arg Glu Val Arg Leu Leu Ala Arg
 195 200 205

Leu Gly Ile Asn Gly Ile Val Cys Gln Gly Tyr Glu Ala Gly Gly His
 210 215 220

Arg Gly Asn Phe Leu Val Asn Asp Pro Lys Asp Asp Glu Asn Leu Ser
 225 230 235 240

Thr Val Gln Leu Val Lys Arg Thr Val Asp Glu Leu Ala Glu Met Lys
 245 250 255

Asn Lys Gly Leu Ile His Ala Thr Pro Phe Val Ile Ala Ala Gly Gly
 260 265 270

Ile Met Asp Ser Lys Asp Ile Ser Tyr Met Leu Ser Gln Gln Ala Asp
 275 280 285

Ala Val Gln Val Gly Thr Ala Phe Leu Gly Cys Ser Glu Ser Asn Ala
 290 295 300

Ser Lys Asn Phe Ser Ser Pro Phe Thr Arg Glu Thr Thr Thr Lys Met
 305 310 315 320

Val Asn Ile Ile Ser Gly Pro Ala Arg Thr Ile Ser Thr Pro Phe
 325 330 335

Ile Glu Lys Val Ile Ala Asn Phe Gln Gly Glu Glu Leu Pro Pro Tyr
 340 345 350

Gly Tyr Met Tyr Ser Ala Phe Lys Gln Val Arg Lys Lys Tyr Pro Glu
 355 360 365

Leu Ala Asn Phe Ile Leu Ala Gly Gln Gly Phe Gln Asn Val Gln Ser
 370 375 380

Gly Ile Thr Thr Asp Lys Lys Ile Glu Thr Met Gly Ala Arg Leu Lys
 385 390 395 400

Ile Val Gly Lys

<210> 43
 <211> 1137
 <212> DNA

<213> Neurospora crassa

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ggccgcctcg	actttccccc	cggtcttcc	cacctaaccg	ccctctctac	cgaactcgcc	240
tccggcccg	gcccgcctcg	tettaaccgc	cgccccctca	ccctctctcc	cggtcttgcc	300
gtcggcctca	ttttaaacca	caccatctcc	gttcccttacg	taaccgacac	cgtcctgccc	360
atcttgcatc	aacactcccc	gcaaggcagtc	tggctttcg	ccaaacgaccc	ggatttcgag	420
gcctttccg	agccctggcg	aaagggaca	gcaaaagcaa	tcatcgagc	ccttcacgct	480
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gagaatcaca	agaagttcaa	ggaggcagcg	agctctgggg	ataactcgcg	ggctgtgact	1020
ttgtccggga	ctgctgtggg	tctgataaaag	gaccagaggc	cggtctggcga	tattgttagg	1080
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<210> 44

<211> 378

<212> PRT

<213> Neurospora crassa

<400> 44

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Ala	Leu	Thr	Lys	Leu	Asn	Ser	Trp	Phe	Pro	Thr	Thr	Lys	Asn	Pro	Val
				20				25				30			

Ile	Ile	Ser	Ala	Pro	Met	Tyr	Leu	Ile	Ala	Asn	Gly	Thr	Leu	Ala	Ala
					35			40				45			

Glu Val Ser Lys Ala Gly Gly Ile Gly Phe Val Ala Gly Gly Ser Asp
 50 55 60

Phe Arg Pro Gly Ser Ser His Leu Thr Ala Leu Ser Thr Glu Leu Ala
 65 70 75 80

Ser Ala Arg Ser Arg Leu Gly Leu Thr Asp Arg Pro Leu Thr Pro Leu
 85 90 95

Pro Gly Ile Gly Val Gly Leu Ile Leu Thr His Thr Ile Ser Val Pro
 100 105 110

Tyr Val Thr Asp Thr Val Leu Pro Ile Leu Ile Glu His Ser Pro Gln
 115 120 125

Ala Val Trp Leu Phe Ala Asn Asp Pro Asp Phe Glu Ala Ser Ser Glu
 130 135 140

Pro Gly Ala Lys Gly Thr Ala Lys Gln Ile Ile Glu Ala Leu His Ala
 145 150 155 160

Ser Gly Phe Val Val Phe Phe Gln Val Gly Thr Val Lys Asp Ala Arg
 165 170 175

Lys Ala Ala Ala Asp Gly Ala Asp Val Ile Val Ala Gln Gly Ile Asp
 180 185 190

Ala Gly Gly His Gln Leu Ala Thr Gly Ser Gly Ile Val Ser Leu Val
 195 200 205

Pro Glu Val Arg Asp Met Leu Asp Arg Glu Phe Lys Glu Arg Glu Val
 210 215 220

Val Val Val Ala Ala Gly Gly Val Ala Asp Gly Arg Gly Val Val Gly
 225 230 235 240

Ala Leu Gly Leu Gly Ala Glu Gly Val Val Leu Gly Thr Arg Phe Thr
 245 250 255

Val Ala Val Glu Ala Ser Thr Pro Glu Phe Arg Arg Lys Val Ile Leu
 260 265 270

Glu Thr Asn Asp Gly Gly Leu Asn Thr Val Lys Ser His Phe His Asp
 275 280 285

Gln Ile Asn Cys Asn Thr Ile Trp His Asn Val Tyr Asp Gly Arg Ala

50

290	295	300
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Val Arg Asn Ala Ser Tyr Asp Asp His Ala Ala Gly Val Pro Phe Glu
305 310 315 320

Glu Asn His Lys Lys Phe Lys Glu Ala Ala Ser Ser Gly Asp Asn Ser
325 330 335

Arg Ala Val Thr Trp Ser Gly Thr Ala Val Gly Leu Ile Lys Asp Gln
340 345 350

Arg Pro Ala Gly Asp Ile Val Arg Glu Leu Arg Glu Ala Lys Glu
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Arg Ile Lys Lys Ile Gln Ala Phe Ala Ala
370 375

<210> 45
<211> 195
<212> PRT
<213> Unknown

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<223> Description of Unknown Organism: A FabK Consensus Sequence

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<222> (2)..(2)
<223> X=Ile or Ala

<220>
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<223> X=any amino acid

<220>
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<223> X=Gly or Ala

<220>
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<223> X=Gly or Pro

<220>
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<223> X=any amino acid and up to 3 may be absent

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<220>
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<222> (169)..(169)
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20	25	30	

Xaa			
35	40	45	

Xaa Xaa Xaa Xaa Xaa Thr Xaa Xaa Pro Phe Xaa Val Xaa Xaa Xaa Xaa			
50	55	60	

Xaa			
65	70	75	80

Xaa			
85	90	95	

Xaa
 100 105 110

Xaa
 115 120 125

Xaa
 130 135 140

Xaa
 145 150 155 160

Xaa Xaa Xaa Xaa Pro Xaa Xaa Xaa Xaa Gly Gly Xaa Xaa Xaa Xaa
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Xaa Xaa Xaa Xaa Ala Xaa Xaa Xaa Leu Gly Ala Xaa Xaa Xaa Xaa
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Gly Thr Arg
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<210> 46
<211> 60
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: A FabK Consensus Sequence

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<223> X=Ile or Val

<220>
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<223> X=any amino acid

<220>
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<222> (5)..(5)
<223> X=Gly or Ala

<220>
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<223> X=Gly or Pro

<220>

<221> MISC_FEATURE
 <222> (8)..(16)
 <223> X=any amino acid and up to 3 may be absent

<220>
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 <222> (18)..(19)
 <223> X=Pro, Ala, Gly, Ser, or Thr

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<220>
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<220>
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 <223> X=any amino acid and up to 6 may be absent

<220>
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 <222> (55)..(55)
 <223> X=Gln, Asn, Glu, or Asp

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 <222> (56)..(56)
 <223> X=any amino acid

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 <222> (59)..(59)
 <223> X=Gly or Ala

<400> 46

Pro	Xaa	Xaa	Xaa	Xaa	Xaa	Met	Xaa								
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			20				25							30	

Xaa															
35							40							45	

Xaa Xaa Xaa Xaa Xaa Thr Xaa Xaa Pro Phe Xaa Val		
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<210> 47
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<212> DNA
<213> Staphylococcus aureus NCTC 8325

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actcaaatgt taagtattga atatccaatt attacagcg gtttgcagg aagtagcacc 180
cccaaaat tagtgcattaaat taataacagt ggtgggttag gcacaatagg cgcatgttac 240
tttaataacgc agcaattgga agatgaaata gattatgtac gccaattaac gtcaattct 300
tttgcgttac atgtctttgt accaagtca caatcatata ccagtagtca aattgaaaat 360
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gtatgttgc ttacttttgg aatttcaacg gaacagatta taagcagggtt gaaagcagcg 540
aatgtcaac ttataggatc agcaacaagt gttgatgaaat ctatcgca tgaaaaagcg 600
ggtatggatc ctatcgatc tcaaggttgtt gaaagcagggtt gacatcgatc ttcattttta 660
aaacctaaaa atcaattacc tatgggttgg acaatatctt tagtgcacaa aattgtat 720
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agtattgtct taggtgcaga aggggtacaa atgggcaccc cattttaac atcacaagac 840
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ataagaaaaag ccgcagcaaa catggcgac aaagagttaa tacatatgtg gatggacaa 1080
agcccgcgac tagcaacaac gcatcccgcc aacaccatca tgtccaatat aatcaatcaa 1140
attaatcaa tcatgtcaataa taaataa 1167

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<211> 355
<212> PRT
<213> Staphylococcus aureus NCTC 8325

<400> 48

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Leu Ile Asn Asn Ser Gly Gly Leu Gly Thr Ile Gly Ala Gly Tyr Phe
 35 40 45

Asn Thr Gln Gln Leu Glu Asp Glu Ile Asp Tyr Val Arg Gln Leu Thr
 50 55 60

Ser Asn Ser Phe Gly Val Asn Val Phe Val Pro Ser Gln Gln Ser Tyr
 65 70 75 80

Thr Ser Ser Gln Ile Glu Asn Met Asn Ala Trp Leu Lys Pro Tyr Arg
 85 90 95

Arg Ala Leu His Leu Glu Glu Pro Val Val Lys Ile Thr Glu Glu Gln
 100 105 110

Gln Phe Lys Cys His Ile Asp Thr Ile Ile Lys Lys Gln Val Pro Val
 115 120 125

Cys Cys Phe Thr Phe Gly Ile Pro Ser Glu Gln Ile Ile Ser Arg Leu
 130 135 140

Lys Ala Ala Asn Val Lys Leu Ile Gly Thr Ala Thr Ser Val Asp Glu
 145 150 155 160

Ala Ile Ala Asn Glu Lys Ala Gly Met Asp Ala Ile Val Ala Gln Gly
 165 170 175

Ser Glu Ala Gly Gly His Arg Gly Ser Phe Leu Lys Pro Lys Asn Gln
 180 185 190

Leu Pro Met Val Gly Thr Ile Ser Leu Val Pro Gln Ile Val Asp Val
 195 200 205

Val Ser Ile Pro Val Ile Ala Ala Gly Gly Ile Met Asp Gly Arg Gly
 210 215 220

Val Leu Ala Ser Ile Val Leu Gly Ala Glu Gly Val Gln Met Gly Thr
 225 230 235 240

Ala Phe Leu Thr Ser Gln Asp Ser Asn Ala Ser Glu Leu Leu Arg Asp
 245 250 255

Ala Ile Ile Asn Ser Lys Glu Thr Asp Thr Val Ile Thr Lys Ala Phe
260 265 270

Ser Gly Lys Leu Ala Arg Gly Ile Asn Asn Arg Phe Ile Glu Glu Met
275 280 285

Ser Gln Tyr Glu Gly Asp Ile Pro Asp Tyr Pro Ile Gln Asn Glu Leu
290 295 300

Thr Ser Ser Ile Arg Lys Ala Ala Ala Asn Ile Gly Asp Lys Glu Leu
305 310 315 320

Ile His Met Trp Ser Gly Gln Ser Pro Arg Leu Ala Thr Thr His Pro
 325 330 335

Ala Asn Thr Ile Met Ser Asn Ile Ile Asn Gln Ile Asn Gln Ile Met
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Gln Tyr Lys
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<210> 50
<211> 250
<212> PRT
<213> FabI Bacillus subtilis

<400> 50

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														15	

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														30	
20															

Ile	Asn	Tyr	Ala	Arg	Ser	Lys	Lys	Ala	Ala	Leu	Glu	Thr	Ala	Glu	Glu
														45	
35															

Ile	Glu	Lys	Leu	Gly	Val	Lys	Val	Leu	Val	Val	Lys	Ala	Asn	Val	Gly
														60	
50															

Gln	Pro	Ala	Lys	Ile	Lys	Glu	Met	Phe	Gln	Gln	Ile	Asp	Glu	Thr	Phe
														80	
65															

Gly	Arg	Leu	Asp	Val	Phe	Val	Asn	Asn	Ala	Ala	Ser	Gly	Val	Leu	Arg
														95	
85															

Pro	Val	Met	Glu	Leu	Glu	Glu	Thr	His	Trp	Asp	Trp	Thr	Met	Asn	Ile
														110	
100															

Asn	Ala	Lys	Ala	Leu	Leu	Phe	Cys	Ala	Gln	Glu	Ala	Ala	Lys	Leu	Met
														125	
115															

Glu	Lys	Asn	Gly	Gly	His	Ile	Val	Ser	Ile	Ser	Ser	Leu	Gly	Ser	
														140	
130															

Ile	Arg	Tyr	Leu	Glu	Asn	Tyr	Thr	Val	Gly	Val	Ser	Lys	Ala	Ala	
														160	
145															

Leu	Glu	Ala	Leu	Thr	Arg	Tyr	Leu	Ala	Val	Glu	Leu	Ser	Pro	Lys	Gln
														175	
165															

Ile	Ile	Val	Asn	Ala	Val	Ser	Gly	Gly	Ala	Ile	Asp	Thr	Asp	Ala	Leu
														190	
180															

Lys	His	Phe	Pro	Asn	Arg	Glu	Asp	Leu	Leu	Glu	Asp	Ala	Arg	Gln	Asn
														205	
195															

Thr	Pro	Ala	Gly	Arg	Met	Val	Glu	Ile	Lys	Asp	Met	Val	Asp	Thr	Val
														220	
210															

Glu Phe Leu Val Ser Ser Lys Ala Asp Met Ile Arg Gly Gln Thr Ile
 225 230 235 240

Ile Val Asp Gly Gly Arg Ser Leu Leu Val
 245 250

<210> 51
 <211> 780
 <212> DNA
 <213> Campylobacter jejuni NCTC 11168 FabI

<400> 51
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 aatgcgc当地 ttgtgtat aatggttcaaa gatttgaga aaaattataa aatcaagct 180
 agagcttatg aattaataat cttagaacctt gaaacctata aagaacttt tgaaaaatt 240
 gatgtggatt ttgatagatgg ggattatttt atctcaaattt ctatcatttc aggacgtgcg 300
 gttttaggtg gctataccaa attttatgtat taaaacccaa aggaaattaa taacatcccc 360
 acagccacag taaaatgtttt tttttgtgggc gcacaagaag cagctaaaag gatggaaaaa 420
 gtaggggggtg gaagcattat ttctatctca tctacaggaa atttagtgc tatagaaaaat 480
 tatttcaggc acgttacacg aaaaagccgtt gtatggactt tggcaagata tgccgtact 540
 gaacttggg aaaaaaatat ccgtgtat gtcgttgcgtt gttggccat taaaactgtat 600
 gttttaagat cttttacaaa ttatgtatggaa gtaaaacagg ctactataaa tttaaacccct 660
 ttaaatcgca tggggcagcc tgaagatgg gtcgttgcgtt gttttttct ttgttcaagt 720
 aaggcaagtt gggttacagg acatacttcc atcgttgcgtt gttgtacaac ttttaataaa 780

<210> 52
 <211> 259
 <212> PRT
 <213> Campylobacter jejuni FabI

<400> 52

Met Asn Thr Glu Phe Gln Gly Lys Thr Leu Val Ile Ser Gly Gly Thr
 1 5 10 15

Arg Gly Ile Gly Lys Ala Ile Val Tyr Glu Phe Ala Lys Val Gly Ala
 20 25 30

Asn Ile Ala Phe Thr Tyr Asn Ser Asn Ala Gln Ile Ala Asp Glu Met
 35 40 45

Val Gln Asp Leu Glu Lys Asn Tyr Lys Ile Lys Ala Arg Ala Tyr Glu
 50 55 60

Phe Asn Ile Leu Glu Pro Glu Thr Tyr Lys Glu Leu Phe Glu Lys Ile
 65 70 75 80

Asp Val Asp Phe Asp Arg Val Asp Tyr Phe Ile Ser Asn Ala Ile Ile
 85 90 95

Ser Gly Arg Ala Val Val Gly Gly Tyr Thr Lys Phe Met Lys Leu Lys
 100 105 110

Pro Lys Gly Ile Asn Asn Ile Phe Thr Ala Thr Val Asn Ala Phe Val
 115 120 125

Val Gly Ala Gln Glu Ala Ala Lys Arg Met Glu Lys Val Gly Gly
 130 135 140

Ser Ile Ile Ser Ile Ser Ser Thr Gly Asn Leu Val Tyr Ile Glu Asn
 145 150 155 160

Tyr Ser Gly His Gly Thr Ala Lys Ala Ala Val Glu Ala Met Ala Arg
 165 170 175

Tyr Ala Ala Thr Glu Leu Gly Glu Lys Asn Ile Arg Val Asn Val Val
 180 185 190

Ser Gly Gly Pro Ile Lys Thr Asp Ala Leu Arg Ala Phe Thr Asn Tyr
 195 200 205

Glu Glu Val Lys Gln Ala Thr Ile Asn Leu Ser Pro Leu Asn Arg Met
 210 215 220

Gly Gln Pro Glu Asp Leu Ala Gly Ala Cys Leu Phe Leu Cys Ser Ser
 225 230 235 240

Lys Ala Ser Trp Val Thr Gly His Thr Phe Ile Val Asp Gly Gly Thr
 245 250 255

Thr Phe Lys

<210> 53
<211> 789
<212> DNA
<213> Helicobacter pylori Fab1

<400> 53
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aataaaaatg ttgaagaagc caacaaaatc atagaagatg tgaggcaaaa atattccatt 120
aaagccaaag cctactctct taatgtttta gagcctgagc aatacacgga gctttcaag 180
caaattgacg ctgtatggat cagagtttttta ctaacgctat tatttatggg 240
cgttctgtcg tgggggatt tgcaccgttt atgcgattaa aacctaaggg gttaaacaac 300
attacacag ccaccgtgtt aegcttcgtc gttaggggctc aagaagccgc aaaacgcatg 360
caaaaaatag gcccgtgggc gatcgtgagc ttaagttcta ccgggaatct agtttatatg 420
cttaattacg ccgggcattgg caattccaaa aacgcgttag aaaccatggt caaatacgc 480
ccgtggatt taggcaatt taacattaga gtgaatgcgg tttagtgcgg gcctattgtat 540
acggacgctt tgaaaggctt ccctgattat gtggagatta aaaaaaaagt agaagagcaa 600
tcgccccctaa aacgcgtggg caatcttaac gatctagccg gagcggctta tttttatgc 660
gatgagaccc aaagcggttg gcttacaggg caaacgatcg ttgttagatgg cgggactact 720
tttaataaa 780

<210> 54

<211> 262

<212> PRT

<213> Helicobacter pylori Fab1

<400> 54

Met	Asn	Gly	Ser	Asn	His	Met	Lys	Asn	Lys	Thr	Leu	Val	Ile	Ser	Gly
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Ala	Thr	Arg	Gly	Ile	Gly	Lys	Ala	Ile	Phe	Val	Arg	Phe	Ala	Gln	Ser
				20				25					30		

Gly	Val	Asn	Ile	Ala	Phe	Thr	Tyr	Asn	Lys	Asn	Val	Glu	Glu	Ala	Asn
				35			40					45			

Lys	Ile	Ile	Glu	Asp	Val	Glu	Gln	Lys	Tyr	Ser	Ile	Lys	Ala	Lys	Ala
	50				55						60				

Tyr	Ser	Leu	Asn	Val	Leu	Glu	Pro	Glu	Gln	Tyr	Thr	Glu	Leu	Phe	Lys
				65			70		75				80		

Gln	Ile	Asp	Ala	Asp	Phe	Asp	Arg	Val	Asp	Phe	Phe	Ile	Ser	Asn	Ala
				85				90					95		

Ile Ile Tyr Gly Arg Ser Val Val Gly Gly Phe Ala Pro Phe Met Arg
 100 105 110

Leu Lys Pro Lys Gly Leu Asn Asn Ile Tyr Thr Ala Thr Val Leu Ala
 115 120 125

Phe Val Val Gly Ala Gln Glu Ala Ala Lys Arg Met Gln Lys Ile Gly
 130 135 140

Gly Gly Ala Ile Val Ser Leu Ser Ser Thr Gly Asn Leu Val Tyr Met
 145 150 155 160

Pro Asn Tyr Ala Gly His Gly Asn Ser Lys Asn Ala Val Glu Thr Met
 165 170 175

Val Lys Tyr Ala Ala Val Asp Leu Gly Glu Phe Asn Ile Arg Val Asn
 180 185 190

Ala Val Ser Gly Gly Pro Ile Asp Thr Asp Ala Leu Lys Ala Phe Pro
 195 200 205

Asp Tyr Val Glu Ile Lys Glu Lys Val Glu Glu Gln Ser Pro Leu Lys
 210 215 220

Arg Met Gly Asn Pro Asn Asp Leu Ala Gly Ala Ala Tyr Phe Leu Cys
 225 230 235 240

Asp Glu Thr Gln Ser Gly Trp Leu Thr Gly Gln Thr Ile Val Val Asp
 245 250 255

Gly Gly Thr Thr Phe Lys
 260

<210> 55
 <211> 843
 <212> DNA
 <213> FabI Streptomyces collinus

<400> 55		
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gcctcgccgc gcatcgccgc caccctggcc ctcaccctcg cccggccgggg tggcacccgtg	120	
gtcgtaact acaaagaagaa cgccgacctg gcacagaaga ccgtcgccga ggtcgaggag	180	
gcccgtggcc agggtttcgcg ggtccaggcg gacgtcgaga ccacccgggg ggtcacccggc	240	
ctgttcgacg aggtggcgca gcgctgcggg aggctcgatc acttcgtctc caacgcggcg	300	

gcgagcgctgt	tcaagaacat	cgtcgatctc	ggcccgacc	acctggaccg	ctcgtacgcg	360
atgaacacctgc	ggcccttcgt	gtggggggcg	caacaggccg	tgaagctgat	ggacaacggc	420
ggacggatcg	tcggcgctgc	ctcttacggc	tcggccggcg	cctacccac	ctacgcatg	480
ctcgccggca	tgaagccgc	catcgactca	tgggtcggt	acatggcggt	ggagtctcgct	540
ccttacggca	tcaacgtcaa	cgcggtcaac	ggcgccctga	tcgactccga	ttagctggag	600
ttttcttaca	acgtcgaggg	catgcccgc	atgcaggcg	tcctcgaccg	catccccggc	660
cgccgtccgg	gcaccgtaca	ggagatggcc	gacaccatcg	ccttctgtct	cgccgacgg	720
gccccgttaca	tcaccggca	gaccctcg	gtcgacggcg	ggctcagcat	cgtcgcgc	780
ccgttcttcg	cggacgcggg	tgaggcgctc	gagctggcc	ccccggcgac	gagagacggc	840
tga						843

<210> 56

<211> 280

<212> PRT

<213> FabI Streptomyces collinus

<400> 56

Met	Asn	Ser	Pro	His	Gln	Gln	Gln	Thr	Ala	Asp	Arg	Arg	Gln	Val	Ser
1					5				10				15		

Leu	Ile	Thr	Gly	Ala	Ser	Arg	Gly	Ile	Gly	Arg	Thr	Leu	Ala	Leu	Thr
				20				25				30			

Leu	Ala	Arg	Arg	Gly	Gly	Thr	Val	Val	Val	Asn	Tyr	Lys	Lys	Asn	Ala
	35				40					45					

Asp	Leu	Ala	Gln	Lys	Thr	Val	Ala	Glu	Val	Glu	Glu	Ala	Gly	Gly	Gln
	50				55				60						

Gly	Phe	Ala	Val	Gln	Ala	Asp	Val	Glu	Thr	Thr	Glu	Gly	Val	Thr	Ala
65					70				75				80		

Leu	Phe	Asp	Glu	Val	Ala	Gln	Arg	Cys	Gly	Arg	Leu	Asp	His	Phe	Val
	85				90			90			95				

Ser	Asn	Ala	Ala	Ala	Ser	Ala	Phe	Lys	Asn	Ile	Val	Asp	Leu	Gly	Pro
	100						105			110					

His	His	Leu	Asp	Arg	Ser	Tyr	Ala	Met	Asn	Leu	Arg	Pro	Phe	Val	Leu
		115					120			125					

Gly	Ala	Gln	Gln	Ala	Val	Lys	Leu	Met	Asp	Asn	Gly	Gly	Arg	Ile	Val
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

130

135

140

Ala Leu Ser Ser Tyr Gly Ser Val Arg Ala Tyr Pro Thr Tyr Tyr Ala Met
145 150 155 160

Leu Gly Gly Met Lys Ala Ala Ile Glu Ser Trp Val Arg Tyr Met Ala
165 170 175

Val Glu Phe Ala Pro Tyr Gly Ile Asn Val Asn Ala Val Asn Gly Gly
180 185 190

Leu Ile Asp Ser Asp Ser Leu Glu Phe Phe Tyr Asn Val Glu Gly Met
195 200 205

Pro Pro Met Gln Gly Val Leu Asp Arg Ile Pro Ala Arg Arg Pro Gly
210 215 220

Thr Val Gln Glu Met Ala Asp Thr Ile Ala Phe Leu Leu Gly Asp Gly
225 230 235 240

Ala Gly Tyr Ile Thr Gly Gln Thr Leu Val Val Asp Gly Gly Leu Ser
245 250 255

Ile Val Ala Pro Pro Phe Phe Ala Asp Ala Gly Glu Ala Leu Glu Leu
 260 265 270

Pro Pro Arg Pro Thr Arg Asp Ala
275 . . 280

<210> 57
<211> 176
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: A FabI Consensus Sequence

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<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> X=Ala, Gly,
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<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> X=Pro, Ala, Gly, Thr, or Ser
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<220>
<221> MISC_FEATURE

<222> (6)..(6)
<223> X=Ile, Val, Leu, or Met

<220>
<221> MISC_FEATURE
<222> (8)..(127)
<223> X=any amino acid and up to 20 may be absent

<220>
<221> MISC_FEATURE
<222> (130)..(130)
<223> X=Glu, Gln, Asn, or Asp

<220>
<221> MISC_FEATURE
<222> (132)..(132)
<223> X=any amino acid

<220>
<221> MISC_FEATURE
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<221> MISC_FEATURE
<222> (136)..(159)
<223> X=any amino acid and up to 6 may be absent

<220>
<221> MISC_FEATURE
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<223> X=any amino acid

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<223> X=Val, Ile, Leu, or Met

<220>
<221> MISC_FEATURE
<222> (172)..(172)
<223> X=Thr, Ala, Ser, Pro, or Gly

<220>
<221> MISC_FEATURE
<222> (173)..(174)

<223> X=any amino acid

<220>
<221> MISC_FEATURE
<222> (175)..(175)
<223> X=Lys, Arg, or His

<400> 57

Gly Xaa Xaa Arg Gly Xaa Gly Xaa
1 5 10 15

Xaa Xaa

Gln Xaa Ala Xaa Lys Xaa Met Xaa Xaa

Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Ala Xaa Glu Xaa Xaa Xaa Xaa Tyr

<212> PR

<213>

<223> Description of Unknown Organism: A FabI Consensus Sequence

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> X=Ala, Gly, Ser, Pro, or Thr

<220>

<221> MISC_FEATURE

<222> (3)..(3)

<223> X=Pro, Ala, Gly, Thr, or Ser

<220>

<221> MISC_FEATURE

<222> (6)..(6)

<223> X=Ile, Val, Leu, or Met

<220>

<221> MISC_FEATURE

<222> (8)..(8)

<223> X=any amino acid

<400> 58

Gly Xaa Xaa Arg Gly Xaa Gly Xaa
1 5

<210> 59

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 59

tctagacata tgaaaacgcg tattacagaa tta

33

<210> 60

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 60

ggatccctaga tactgggcac cttgacc

27

<210> 61

<211> 5

<212> PRT

<213> Unknown

<220>
<223> Description of Unknown Organism: A SDR Consensus Sequence

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<222> (2)..(4)
<223> X=any amino acid

<400> 61

Tyr Xaa Xaa Xaa Lys
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<210> 62
<211> 8
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: A Enoyl Reductase Consensus Sequence

<220>
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<222> (2)..(7)
<223> X=any amino acid

<400> 62

Thr Xaa Xaa Xaa Xaa Xaa Xaa Lys
1 5